

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2005, 23:54:06 ; Search time 165 Seconds
(without alignments)
53.912 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGPGQARGFGPTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	23	8	ADN12242
2	132	100.0	24	8	ADN12248
3	132	100.0	24	8	ADN12245
4	132	100.0	24	8	ADN12247
5	132	100.0	24	8	ADN12246
6	132	100.0	84	8	ADN12240
7	132	100.0	84	8	ADN12251
8	132	100.0	85	8	ADN12250
9	132	100.0	243	8	ADQ18267
10	132	100.0	1014	7	ADC21544
11	132	100.0	1417	8	ABM83560
12	132	100.0	1418	2	AAR59751
13	132	100.0	1418	2	AAR71703
14	132	100.0	1418	3	AAY96124
15	132	100.0	1418	3	AAB35624
16	132	100.0	1418	5	AAB35624
17	132	100.0	1418	5	ABB80735
18	132	100.0	1418	5	ABG93927
19	132	100.0	1418	5	ABO9627
20	132	100.0	1418	7	ADF13077
21	132	100.0	1420	8	ADP48530
22	132	100.0	1487	2	AAW61562
23	132	100.0	1487	5	ABG61861
24	132	100.0	1487	6	ABP56769
25	122	92.4	1014	7	ADC21591

26	122	92.4	1419	7	AD555694	Ad555694 Rat Prote
27	122	92.4	1487	5	ABG93928	ABG93928 Mouse pol
28	117	88.6	1442	2	AAR79480	AAR79480 Rat type
29	115	87.1	102	4	AAB68055	AAB68055 Amino aci
30	115	87.1	102	4	AAE02701	AAE02701 Human alp
31	115	87.1	102	7	ADB84288	ADB84288 Recombina
32	115	87.1	130	4	ABU53017	ABU53017 Human tes
33	115	87.1	134	4	ABU53021	ABU53021 Human tes
34	115	87.1	154	4	ABU53012	ABU53012 Human tes
35	115	87.1	261	4	AAE02702	AAE02702 Human alp
36	115	87.1	261	7	ADB84289	ADB84289 Recombina
37	115	87.1	294	7	ADB87060	ADB87060 Human pan
38	115	87.1	310	2	AAY06238	AAY06238 Mouse rec
39	115	87.1	501	4	AAE02703	AAE02703 Human alp
40	115	87.1	501	7	ADB84290	ADB84290 Recombina
41	115	87.1	595	2	AAY06239	AAY06239 Mouse rec
42	115	87.1	614	7	ADB87059	ADB87059 Human pan
43	115	87.1	615	7	ADB87063	ADB87063 Human pan
44	115	87.1	691	7	ADB87058	ADB87058 Human pan
45	115	87.1	822	2	AAY06240	AAY06240 Mouse rec

ALIGNMENTS

RESULT 1

ADN12242
ID ADN12242 standard; peptide; 23 AA.

AC ADN12242;

DT 01-JUL-2004 (first entry)

DE Type II collagen degradation rate altering peptide CB12-II.

XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.

OS Synthetic.

PN WO2004031206-A2.

XX 15-APR-2004.

XX 30-SEP-2003; 2003WO-US030744.

XX 30-SEP-2002; 2002US-0414332P.

XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

PI Poole AR;

XX WPI; 2004-316460/29.

XX New peptides that regulate the degradation of type II collagen, useful
PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
PT eye diseases.

XX Claim 1; Page 50; 74pp; English.

XX The invention relates to an isolated or purified peptide comprising a
XX fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
XX CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
XX substituted variant, mimetic, inhibitor or homologue. The peptide alters
XX the rate of degradation of type II collagen or the rate of chondrocyte
XX hypertrophy. The peptide or its fragment is hydroxylated at one or more
XX of the proline or lysine residues of the peptide. A pharmaceutical
XX composition comprising a pharmaceutical carrier and at least one of the
XX peptide inhibitors cited above, is useful for reducing collagen matrix
XX turnover in mammals, particularly humans, or for reducing degradation of
XX one or more collagen proteins. An isolated or purified antibody that
XX specifically binds to an epitope of the peptide or its antigenic fragment

CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 132; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
 DB 1 ERGPPGPGQARGFGTGTGLPGVK 23

RESULT 2
 ADN12248
 ID ADN12248 standard; peptide; 24 AA.
 XX
 AC ADN12248;
 XX
 DF 01-JUL-2004 (first entry)
 XX
 XX Type II collagen degradation rate altering peptide Pro21.
 DE
 XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 15 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"

XX WO2004031206-A2.
 XX 15-APR-2004.
 XX 30-SEP-2003; 2003WO-US030744.
 XX 30-SEP-2002; 2002US-0414332P.
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX
 XX Poole AR;
 XX WPI; 2004-316460/29.
 XX
 XX New peptides that regulate the degradation of type II collagen, useful
 PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 PT eye diseases.
 XX
 XX Claim 1; Page 50; 74pp; English.

XX The invention relates to an isolated or purified peptide comprising a
 CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 CC substituted variant, mimetic, inhibitor or homologue. The peptide alters

CC the rate of degradation of type II collagen or the rate of chondrocyte
 CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
 DB 2 ERGPPGPGQARGFGTGTGLPGVK 24

RESULT 3
 ADN12245
 ID ADN12245 standard; peptide; 24 AA.
 XX
 AC ADN12245;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 XX Type II collagen degradation rate altering peptide Pro6.
 DE
 XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 15 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"

XX WO2004031206-A2.
 XX 15-APR-2004.
 XX 30-SEP-2003; 2003WO-US030744.
 XX 30-SEP-2002; 2002US-0414332P.
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX
 XX Poole AR;
 XX WPI; 2004-316460/29.

XX New peptides that regulate the degradation of type II collagen, useful
 PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or

PT eye diseases.
 XX
 PS Claim 1; Page 50; 74pp; English.
 XX
 CC The invention relates to an isolated or purified peptide comprising a
 CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 CC the rate of degradation of type II collagen or the rate of chondrocyte
 CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
 Db |||||
 2 ERGPPGPGQARGFGPTGGLPGVK 24
 RESULT 4
 ADN12247
 ID ADN12247 standard; peptide; 24 AA.
 AC ADN12247;
 XX
 XX 01-JUL-2004 (first entry)
 XX
 XX Type II collagen degradation rate altering peptide Pro18.
 DE
 XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 15 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"
 FT
 XX WO2004031206-A2.
 PN
 XX 15-APR-2004.
 PD
 XX 30-SEP-2003; 2003WO-US030744.
 PF
 XX 30-SEP-2002; 2002US-0414332P.
 PR
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

XX Poole AR;
 PI
 XX WPI; 2004-316460/29.
 DR
 XX New peptides that regulate the degradation of type II collagen, useful
 PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 PT eye diseases.
 XX
 PS Claim 1; Page 50; 74pp; English.
 XX
 CC The invention relates to an isolated or purified peptide comprising a
 CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 CC the rate of degradation of type II collagen or the rate of chondrocyte
 CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
 Db |||||
 2 ERGPPGPGQARGFGPTGGLPGVK 24
 RESULT 5
 ADN12246
 ID ADN12246 standard; peptide; 24 AA.
 XX
 XX ADN12246;
 AC
 XX 01-JUL-2004 (first entry)
 XX
 XX Type II collagen degradation rate altering peptide Pro15.
 DE
 XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"
 FT
 XX WO2004031206-A2.
 PN

XX PD 15-APR-2004.
 XX PF 30-SEP-2003; 2003WO-US030744.
 XX PF 30-SEP-2002; 2002US-0414332P.
 XX PR (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX PA Poole AR;
 XX PI WPI; 2004-316460/29.
 XX DR
 XX PT New peptides that regulate the degradation of type II collagen, useful
 XX PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 XX PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 XX PT eye diseases.
 XX PS
 XX PS Claim 1; Page 50; 74pp; English.
 XX CC The invention relates to an isolated or purified peptide comprising a
 XX CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 XX CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 XX CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 XX CC the rate of degradation of type II collagen or the rate of chondrocyte
 XX CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 XX CC of the proline or lysine residues of the peptide. A pharmaceutical
 XX CC composition comprising a pharmaceutical carrier and at least one of the
 XX CC peptide inhibitors cited above, is useful for reducing collagen matrix
 XX CC turnover in mammals, particularly humans, or for reducing degradation of
 XX CC one or more collagen proteins. An isolated or purified antibody that
 XX CC specifically binds to an epitope of the peptide or its antigenic fragment
 XX CC is used to inhibit the activity of the peptide, to identify inhibitors of
 XX CC the generation of the peptide, or to identify a subject at risk for rapid
 XX CC or slow progression of a disease responding to therapy designed to arrest
 XX CC cartilage degradation or at risk for a disease by showing of early pre-
 XX CC clinical changes prior to clinical presentation of the disease, where the
 XX CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 XX CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 XX CC addition, the antibody is used to detect the release of type II collagen
 XX CC degradation products in body fluids, e.g. tissue extracts, serum,
 XX CC synovial fluid or urine. The composition and methods may be used for
 XX CC diagnosing and treating such diseases. The present sequence represents a
 XX CC specific example of the peptide effective in altering the rate of
 XX CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX SQ
 XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGQARGFGCTGGLPGVK 23
 Db 2 ERGPPGQARGFGCTGGLPGVK 24
 RESULT 6
 ADN12240
 ID ADN12240 standard; peptide; 84 AA.
 XX AC
 XX AC ADN12240;
 XX DT 01-JUL-2004 (first entry)
 XX DE Type II collagen degradation rate altering peptide.
 XX KW Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 XX KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX OS Synthetic.
 XX XX
 XX PN WO2004031206-A2.

XX PD 15-APR-2004.
 XX PF 30-SEP-2003; 2003WO-US030744.
 XX PF 30-SEP-2002; 2002US-0414332P.
 XX PR (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX PA Poole AR;
 XX PI WPI; 2004-316460/29.
 XX DR
 XX PT New peptides that regulate the degradation of type II collagen, useful
 XX PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 XX PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 XX PT eye diseases.
 XX PS
 XX PS Disclosure; Page 9; 74pp; English.
 XX CC The invention relates to an isolated or purified peptide comprising a
 XX CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 XX CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 XX CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 XX CC the rate of degradation of type II collagen or the rate of chondrocyte
 XX CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 XX CC of the proline or lysine residues of the peptide. A pharmaceutical
 XX CC composition comprising a pharmaceutical carrier and at least one of the
 XX CC peptide inhibitors cited above, is useful for reducing collagen matrix
 XX CC turnover in mammals, particularly humans, or for reducing degradation of
 XX CC one or more collagen proteins. An isolated or purified antibody that
 XX CC specifically binds to an epitope of the peptide or its antigenic fragment
 XX CC is used to inhibit the activity of the peptide, to identify inhibitors of
 XX CC the generation of the peptide, or to identify a subject at risk for rapid
 XX CC or slow progression of a disease responding to therapy designed to arrest
 XX CC cartilage degradation or at risk for a disease by showing of early pre-
 XX CC clinical changes prior to clinical presentation of the disease, where the
 XX CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 XX CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 XX CC addition, the antibody is used to detect the release of type II collagen
 XX CC degradation products in body fluids, e.g. tissue extracts, serum,
 XX CC synovial fluid or urine. The composition and methods may be used for
 XX CC diagnosing and treating such diseases. The present sequence represents a
 XX CC peptide effective in altering the rate of degradation of type II collagen
 XX CC or the rate of chondrocyte hypertrophy.
 XX SQ
 XX SQ Sequence 84 AA;
 Query Match 100.0%; Score 132; DB 8; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGQARGFGCTGGLPGVK 23
 Db 25 ERGPPGQARGFGCTGGLPGVK 47
 RESULT 7
 ADN12251
 ID ADN12251 standard; peptide; 84 AA.
 XX AC
 XX AC ADN12251;
 XX DT 01-JUL-2004 (first entry)
 XX DE Type II collagen degradation rate altering peptide.
 XX KW Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 XX KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX OS Synthetic.
 XX XX
 XX XX Location/Qualifiers

FT Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 9
 FT Modified-site 12 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"
 FT Modified-site 30 /note= "hydroxylated proline"
 FT Modified-site 39 /note= "hydroxylated proline"
 FT Modified-site 42 /note= "hydroxylated proline"
 FT Modified-site 45 /note= "hydroxylated proline"
 FT Modified-site 66 /note= "hydroxylated proline"
 FT Modified-site 75 /note= "hydroxylated proline"
 FT Modified-site 81 /note= "hydroxylated proline"
 FT Modified-site 81 /note= "hydroxylated proline"
 XX WO2004031206-A2.
 XX 15-APR-2004.
 XX 30-SEP-2003; 2003WO-US030744.
 XX 30-SEP-2002; 2002US-0414332P.
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX Poole AR;
 XX WPI; 2004-316460/29.
 XX New peptides that regulate the degradation of type II collagen, useful for diagnosing and treating for e.g. osteoarthritis, rheumatoid arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or eye diseases.
 XX Disclosure; Fig 1; 74pp; English.
 XX The invention relates to an isolated or purified peptide comprising a fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III, CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively substituted variant, mimetic, inhibitor or homologue. The peptide alters the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy. The peptide or its fragment is hydroxylated at one or more of the proline or lysine residues of the peptide. A pharmaceutical composition comprising a pharmaceutical carrier and at least one of the peptide inhibitors cited above, is useful for reducing collagen matrix turnover in mammals, particularly humans, or for reducing degradation of one or more collagen proteins. An isolated or purified antibody that specifically binds to an epitope of the peptide or its antigenic fragment is used to inhibit the activity of the peptide, to identify inhibitors of the generation of the peptide, or to identify a subject at risk for rapid or slow progression of a disease responding to therapy designed to arrest cartilage degradation or at risk for a disease by showing of early pre-clinical changes prior to clinical presentation of the disease, where the disease is selected from osteoarthritis, rheumatoid arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In addition, the antibody is used to detect the release of type II collagen degradation products in body fluids, e.g. tissue extracts, serum, synovial fluid or urine. The composition and methods may be used for diagnosing and treating such diseases. The present sequence represents a peptide effective in altering the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX Sequence 84 AA;
 XX Query Match 100.0%; Score 132; DB 8; Length 84;

Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGARGPFGTGLPGVK 23
 DB 26 ERGPPGPGARGPFGTGLPGVK 48
 RESULT 8
 ADN12250
 ID ADN12250 standard; peptide; 85 AA.
 XX AC ADN12250;
 XX 01-JUL-2004 (first entry)
 XX Type II collagen degradation rate altering peptide CB12.
 XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 9 /note= "hydroxylated proline"
 FT Modified-site 12 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"
 FT Modified-site 30 /note= "hydroxylated proline"
 FT Modified-site 39 /note= "hydroxylated proline"
 FT Modified-site 42 /note= "hydroxylated proline"
 FT Modified-site 45 /note= "hydroxylated proline"
 FT Modified-site 66 /note= "hydroxylated proline"
 FT Modified-site 75 /note= "hydroxylated proline"
 FT Modified-site 81 /note= "hydroxylated proline"
 FT Modified-site 81 /note= "hydroxylated proline"
 XX WO2004031206-A2.
 XX 15-APR-2004.
 XX 30-SEP-2003; 2003WO-US030744.
 XX 30-SEP-2002; 2002US-0414332P.
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX Poole AR;
 XX WPI; 2004-316460/29.
 XX New peptides that regulate the degradation of type II collagen, useful for diagnosing and treating for e.g. osteoarthritis, rheumatoid arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or eye diseases.
 XX Disclosure; Fig 1; 74pp; English.
 XX The invention relates to an isolated or purified peptide comprising a fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III, CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively substituted variant, mimetic, inhibitor or homologue. The peptide alters the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy. The peptide or its fragment is hydroxylated at one or more of the proline or lysine residues of the peptide. A pharmaceutical composition comprising a pharmaceutical carrier and at least one of the peptide inhibitors cited above, is useful for reducing collagen matrix turnover in mammals, particularly humans, or for reducing degradation of one or more collagen proteins. An isolated or purified antibody that specifically binds to an epitope of the peptide or its antigenic fragment is used to inhibit the activity of the peptide, to identify inhibitors of the generation of the peptide, or to identify a subject at risk for rapid or slow progression of a disease responding to therapy designed to arrest cartilage degradation or at risk for a disease by showing of early pre-clinical changes prior to clinical presentation of the disease, where the disease is selected from osteoarthritis, rheumatoid arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In addition, the antibody is used to detect the release of type II collagen degradation products in body fluids, e.g. tissue extracts, serum, synovial fluid or urine. The composition and methods may be used for diagnosing and treating such diseases. The present sequence represents a peptide effective in altering the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX Sequence 84 AA;
 XX Query Match 100.0%; Score 132; DB 8; Length 84;

CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 CC
 SQ Sequence 85 AA;

Query Match 100.0%; Score 132; DB 8; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGFGPTGGLPGVK 23
 Db 26 ERGPPGQARGFGPTGGLPGVK 48

RESULT 9
 ADQ18267
 ID ADQ18267 standard; protein; 243 AA.
 XX ADQ18267;

XX 26-AUG-2004 (first entry)
 DT Human soft tissue sarcoma-upregulated protein - SEQ ID 1085.
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW Homo sapiens.
 OS WO2004048938-A2.
 PN 10-JUN-2004.
 XX 26-NOV-2003; 2003WO-US038193.
 PF 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 DR
 XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX Example 2; SEQ ID NO 1085; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.

XX Sequence 243 AA;

Query Match 100.0%; Score 132; DB 8; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGFGPTGGLPGVK 23
 Db 167 ERGPPGQARGFGPTGGLPGVK 189

RESULT 10
 ADC21544
 ID ADC21544 standard; protein; 1014 AA.

XX AC ADC21544;

XX DT 18-DEC-2003 (first entry)

XX DE Human type II collagen protein sequence.

XX triple helix formation sequence; interpolyptide linkage;
 KW rheumatoid arthritis; autoimmune disease; inflammatory disease;
 KW peripheral joint; major histocompatibility complex class II region;
 KW HLA-DR; T cell; joint specific antigen; B cell; type II collagen; CII;
 KW antiarthritic; antirheumatic; immunosuppressive; dermatological;
 KW antiinflammatory; antipsoriatic; antiasthmatic; neuroprotective;
 KW relapsing polycondritis; systemic lupus erythematosus; psoriasis;
 KW asthma; Sjogren's syndrome; multiple sclerosis; human.

XX Homo sapiens.

XX WO2003006603-A2.

XX 23-JAN-2003.

XX 11-JUL-2002; 2002WO-IB004256.

XX 12-JUL-2001; 2001US-0305048P.

XX (AREX-) AREXIS AB.

XX Holmdahl R, Burkhardt H, Engstrom JA, Kihlberg J;

XX WPI; 2003-221724/21.

XX N-PSDB; ADC21545.

XX Composition for treating autoimmune disorders such as rheumatoid
 PT arthritis, comprises three polypeptides, each comprising a triple helix
 PT formation sequence, and at least two interpolyptide linkages.

XX Disclosure; SEQ ID NO 1; 113pp; English.

XX This invention relates to a novel composition comprising three
 CC polypeptides, where each polypeptide comprises a triple helix formation
 CC sequence and at least two interpolyptide linkages such that each
 CC polypeptide is attached to at least one of the other two polypeptides.
 CC Rheumatoid arthritis is an autoimmune, inflammatory disease that affects
 CC peripheral joints. The main genetic association is to the major
 CC histocompatibility complex class II region (HLA-DR), suggesting that T
 CC cell mediated autoimmune recognition of joint specific antigens is
 CC involved in the disease. In addition, B cell mediated autoimmune
 CC responses have been observed in rheumatoid joints. Specifically, B cells
 CC have been detected secreting IGF antibodies specific for type II collagen
 CC (CII). The compounds of the invention may be antiarthritic,

CC antirheumatic, immunosuppressive, dermatological, antiinflammatory,
 CC antipsoriatic, antiashmatic or vasoprotective through the enhancement of
 CC tolerance to the endogenous polypeptide. The compounds may be useful for
 CC diagnosing and treating autoimmune conditions such as rheumatoid
 CC arthritis, relapsing polychondritis, systemic lupus erythematosus,
 CC psoriasis, chronic stages of aschma, Jorge's syndrome and multiple
 CC sclerosis. The present sequence is that of the human type II collagen
 CC (CII) protein which was used to identify the peptide epitopes of the
 CC invention.
 XX
 SQ Sequence 1014 AA;

Query Match 100.0%; Score 132; DB 7; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPPTGGLPGVK 23
 DB 65 ERGPPGPGARGPPTGGLPGVK 87

RESULT 11
 AEM83560
 ID AEM83560 standard; protein; 1417 AA.

XX
 AC AEM83560;

XX
 DT 18-NOV-2004 (first entry)

XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3809.

XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX
 OS Homo sapiens.

XX
 PN WO2004023973-A2.

XX
 PD 25-MAR-2004.

XX
 PF 12-SEP-2003; 2003WO-US028227.

XX
 PR 12-SEP-2002; 2002US-0410259P.

XX
 PR 12-SEP-2002; 2002US-0410260P.

XX
 PA (INCY-) INCYTE CORP.

XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX
 DR WPI: 2004-329368/30.

XX
 DR N-PSDB; ACN42212.

XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

XX
 PS Claim 27; Page; 190pp; English.

XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for sonatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 1417 AA;

Query Match 100.0%; Score 132; DB 8; Length 1417;
 Best Local Similarity 100.0%; Pred. No. 3.5e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPPTGGLPGVK 23
 DB 265 ERGPPGPGARGPPTGGLPGVK 287

RESULT 12

AAR59751
 ID AAR59751 standard; protein; 1418 AA.

XX
 AC AAR59751;

XX
 DT 25-MAR-2003 (revised)

XX
 DT 14-FEB-1995 (first entry)

XX
 DE Type II collagen.

XX
 KW Collagen; triple helix; articular cartilage; collagenase; degradation;
 KW monoclonal antibody; epitope; matrix; metalloproteinase.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

XX
 FT Peptide 1..24

XX
 FT /label= Signal peptide.

XX
 PN WO9414070-A1.

XX
 PD 23-JUN-1994.

XX
 PF 06-DEC-1993; 93WO-CA000522.

XX
 PF 04-DEC-1992; 92US-00984123.

XX
 PR (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.

XX
 PI Poole AR, Hollander AP;

XX
 PI WPI: 1994-234222/28.

XX
 DR Determn. of cartilage degradation - using a monoclonal antibody to

XX
 PT measure the amt. of unwound collagen or fragments in samples.

XX
 PT Disclosure; Fig 1; 119pp; English.

XX
 PS Type II collagen constitutes the bulk of the fibrillar backbone of

XX
 CC cartilage matrix. It is composed of a tightly wound triple helix which
 CC can only be cleaved by the metalloproteinase collagenase to produce 3/4
 CC and 1/4 length alpha chain fragments. The destruction of articular
 CC cartilage is due, in part, to the degradation of collagen. Incapable of
 CC maintaining its helical structure at physiological temperatures,
 CC collagenase-cleaved collagens unwind and become susceptible to further
 CC degradation by other proteinases. By producing monoclonal antibodies
 CC directed against epitopes which are only revealed when collagen is
 CC unwound, the antibodies provide a means of determining the degradation of
 CC cartilage in a biological sample. The antibodies do not bind to native
 CC helical collagen. Epitopes used in the production of such antibodies are
 CC described in AAR59749, AAR59750 and AAR67742. (Updated on 25-MAR-2003 to
 CC correct PN field.)


```

XX SQ Sequence 1418 AA;
    Query Match 100.0%; Score 132; DB 2; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 13
AAR71703
ID AAR71703 standard; protein; 1418 AA.
XX
AC AAR71703;
XX
DT 25-MAR-2003 (revised)
DT 17-OCT-1995 (first entry)
XX
DE Collagen alpha 1 (II) chain precursor.
XX
KW Collagen; antibody; immunoassay; metabolism; diagnosis; monitoring;
KW disorder; osteoporosis; metastatic progression; Paget's disease;
KW hyperthyroidism; bone; resorption; rheumatoid arthritis; osteoarthritis;
KW vasculitis syndrome.
XX
OS Homo sapiens.
XX
PN WO9508115-A1.
XX
PD 23-MAR-1995.
XX
PF 19-SEP-1994; 94WO-DK000348.
XX
PR 17-SEP-1993; 93DK-00001040.
XX
PA (OSTE-) OSTEOMETER AS.
XX
PI Qvist P, Bonde M;
XX
XX WPI; 1995-131456/17.
XX
PT Assaying collagen fragments in body fluid by immunoassay - using
PT antibodies raised against synthetic peptide(s) contg. potential
PT crosslinking sites, to diagnose and monitor disorders of collagen
PT metabolism, e.g. osteoporosis.
XX
PS Disclosure (Appendix A); Page 53; 87pp; English.
XX
CC Determination of collagen fragments in body fluids can be achieved by
CC immunoassay using antibodies directed against synthetic peptides derived
CC from collagen which contain sites of potential crosslinking. The method
CC is used to diagnose and monitor treatment of disorders of collagen
CC metabolism (degradation of type I collagen may indicate osteoporosis,
CC metastatic progression, Paget's disease, hyperthyroidism or other
CC conditions involving excessive bone resorption; degradation of type II
CC collagen may indicate rheumatoid arthritis or osteoarthritis; and of type
CC III collagen, vaculitis syndrome). The method can also be used to assess
CC the toxicity of a compound and to test drugs for their effect on collagen
CC metabolism. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 1418 AA;

    Query Match 100.0%; Score 132; DB 2; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 14
AAY96124
ID AAY96124 standard; peptide; 1418 AA.
XX
AC AAY96124;
XX
DT 19-DEC-2000 (first entry)
DE Collagen type II alpha-1.
XX
KW Collagen type II; rheumatoid arthritis; osteoarthritis; assay; diagnosis.
XX
OS Homo sapiens.
XX
PN US6110689-A.
XX
PD 29-AUG-2000.
XX
PF 04-NOV-1997; 97US-00963825.
XX
PR 21-JAN-1994; 94US-00187319.
XX
XX (OSTE-) OSTEOMETER AS.
XX
PI Bonde M, Qvist P;
XX
XX WPI; 2000-586349/55.
XX
PT Assaying type I collagen fragments for diagnosing osteoporosis in
PT postmenopausal woman, involves contacting body fluid with synthetic
PT collagen peptide and antibody and quantifying by competitive binding
PT assay.
XX
PS Disclosure; Col 37-46; 41pp; English.
XX
CC The present sequence is that of human type II collagen alpha-1. The
CC invention is based on the discovery of the presence of particular
CC collagen fragments in body fluids of patients compared with those of
CC healthy subjects. These fragments are generated upon collagen degradation
CC and are partly characterised by the presence of potential sites for
CC crosslinking. A method for assaying collagen fragments in a body fluid
CC sample is based on the competitive binding to immunological binding
CC partners of collagen fragments in the sample and of synthetic peptides
CC derived from collagen and containing crosslinkable sites (see AAY96112-
CC 17). When considering the degradation of type II collagen, the assay can
CC be used as a means of identifying the presence of rheumatoid arthritis
CC and osteoarthritis
XX
SQ Sequence 1418 AA;

    Query Match 100.0%; Score 132; DB 3; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 15
AAB35624
ID AAB35624 standard; protein; 1418 AA.
XX
AC AAB35624;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human type II collagen.
XX
KW Type II collagen; arthritis; joint; ds.
XX
OS Homo sapiens.

```



```
XX US6132976-A.
PN
XX
XX PD 17-OCT-2000.
XX
XX PF 22-JAN-1998; 98US-00010999.
XX
XX PR 04-DEC-1992; 92US-00984123.
XX PR 17-JUL-1995; 95US-00448501.
XX
XX PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
XX
XX PI Billinghamurst RC, Poole AR, Hollander AP;
XX
XX WPI; 2001-006136/01.
XX
XX PT Detecting cartilage degradation useful for early detection of arthritis
PT or joint damage by contacting the biological sample with an antibody that
PT binds to an epitope of unwound type II collagen chains but not to a
PT native helical collagen.
XX
XX PS Example 1; Fig 1; 58pp; English.
XX
XX CC The present invention relates to detecting cartilage degradation in a
CC biological sample by identifying the presence of unwound type II collagen
CC in the sample. The method involves contacting the sample with a
CC monoclonal antibody which only binds an epitope on unwound type II
CC collagen chains. The invention is useful for the early detection of
CC arthritis and joint damage and for monitoring disease related to collagen
XX
XX SQ Sequence 1418 AA;
Query Match 100.0%; Score 132; DB 4; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db |||||
196 ERGPPGPGQARGPFGTGLPGVK 218

Search completed: October 8, 2005, 00:23:36
Job time : 167 secs
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Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 00:06:37 ; Search time 39 Seconds
(without alignments)
56.743 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPCPQARGFPPTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database :

PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	673	1 CGBO6C	collagen alpha 1(I
2	132	100.0	1418	2 T45467	collagen alpha 1(I
3	132	100.0	1486	1 B40333	collagen alpha 1(I
4	132	100.0	1487	1 CGHU6C	collagen alpha 1(I
5	132	100.0	1492	2 A40333	collagen alpha 1(I
6	122	92.4	1419	2 A41182	collagen alpha 1(I
7	122	92.4	1487	2 B41182	collagen alpha 1(I
8	118	89.4	402	1 CGBO2S	collagen alpha 2(I
9	115	87.1	779	1 CGBO1S	collagen alpha 1(I
10	115	87.1	1453	2 S21626	collagen alpha 1(I
11	115	87.1	1454	1 CGHU1S	collagen alpha 1(I
12	112	84.8	140	2 A05249	collagen alpha 1(I
13	112	84.8	671	1 CGRT1S	collagen alpha 1(I
14	112	84.8	1042	1 CGCH1S	collagen alpha 1(I
15	109	82.6	1366	1 CGHU2S	collagen alpha 2(I
16	109	82.6	1373	1 A43291	collagen alpha 2(I
17	103	78.0	964	1 CGCH2S	collagen alpha 2(I
18	94	71.2	1532	2 A61262	collagen alpha 1(X
19	94	71.2	2944	2 A54849	collagen alpha 1(V
20	93.	70.5	1659	1 CGM54B	collagen alpha 1(I
21	92	69.7	1690	1 CGHU1B	collagen alpha 4(I
22	92	69.7	1691	1 S22917	collagen alpha 5(I
23	92	69.7	1763	2 S16366	collagen alpha 2(I
24	91	68.9	299	2 T29556	hypothetical prote
25	91	68.9	1669	1 CGHU4B	collagen alpha 1(I
26	90	68.2	518	2 A55840	macrophage bacteri
27	90	68.2	920	2 A45748	collagen alpha 1(V
28	90	68.2	1549	2 I48103	type VII collagen
29	88	66.7	177	2 S37749	collagen alpha 2(X

30	88	66.7	210	2 B44984	collagen - nematod
31	88	66.7	307	2 T19582	hypothetical prote
32	88	66.7	330	2 S46657	collagen alpha 1(X
33	88	66.7	675	2 S20819	collagen alpha 3(I
34	87	65.9	423	2 A41207	collagen 13, nonfi
35	87	65.9	438	2 S53787	collagen alpha cha
36	87	65.9	636	2 S41067	collagen alpha 1(I
37	87	65.9	921	2 S40495	collagen alpha 1(I
38	87	65.9	921	2 S42617	collagen alpha 1(I
39	87	65.9	1464	2 S59856	collagen alpha 1(I
40	87	65.9	1712	1 CGHU2B	collagen alpha 2(I
41	86	65.2	284	2 T28887	collagen dpy-10 -
42	86	65.2	453	2 S18804	collagen alpha 4(I
43	85	64.4	283	2 T29837	hypothetical prote
44	85	64.4	294	2 T29838	hypothetical prote
45	85	64.4	294	2 T29839	hypothetical prote

ALIGNMENTS

RESULT 1

CGBO6C

collagen alpha 1(II) chain precursor - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence revision 17-May-1996 #text change 09-Jul-2004

C;Accession: A90369; A90396; A92210; S03940; A90189; A05039; A02859

R;Miller, E.J.; Lunde, L.G.

Biochemistry 12, 3153-3159, 1973

A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
A;Reference number: A90369; MUID:73258693; PMID:4732855

A;Contents: composition of CNBr1 and CNBr4

A;Accession: A90369

A;Molecule type: protein

A;Residues: 1-15 <MFL>

A;Cross-references: UNIPROT:P02459

A;Experimental source: cartilage

A;Note: residues positioned by comparison with human alpha 1(II) chain

R;Butler, W.T.; Miller, E.J.; Finch Jr., J.E.

Biochemistry 15, 3000-3006, 1976

A;Title: The covalent structure of cartilage collagen. Amino acid sequence of the NH-2-
A;Reference number: A90396; MUID:76253504; PMID:782511

A;Contents: fragments CNBr2 (16-18), CNBr3 (19-21), CNBr6 (22-54), CNBr12 (55-138), and

A;Accession: A90396

A;Molecule type: protein

A;Residues: 16-177 <BUT>

A;Experimental source: cartilage

A;Note: order of CNBr peptides determined

R;Butler, W.T.; Finch Jr., J.E.; Miller, E.J.

J. Biol. Chem. 252, 639-643, 1977

A;Title: The covalent structure of cartilage collagen. Evidence for sequence heterogene
A;Reference number: A92210; MUID:77093864; PMID:833147

A;Accession: A92210

A;Molecule type: protein

A;Residues: 139-178, 'Z', 180-184, 'PA', 187-190, 'AS', 193-194, 'T', 196-198 <BU2>

A;Experimental source: cartilage

A;Note: a minor, probably nonallelic, alpha 1(II) component has 143-Ala, 164-Leu, and p

R;Seyer, J.M.; Hasty, K.A.; Kang, A.H.

Eur. J. Biochem. 181, 159-173, 1989

A;Title: Covalent structure of collagen. Amino acid sequence of an arthritogenic cyanog
A;Reference number: S03940; MUID:89231683; PMID:2714276

A;Accession: S03940

A;Molecule type: protein

A;Residues: 139-417 <SEY>

R;Butler, W.T.; Miller, E.J.; Finch Jr., J.E.; Inagami, T.

Biochem. Biophys. Res. Commun. 57, 190-195, 1974

A;Title: Homologous regions of collagen alpha1 (I) and alpha1(II) chains: apparent clus
A;Reference number: A90189; MUID:74163168; PMID:4857180

A;Accession: A90189

A;Molecule type: protein

A;Residues: 418-492 <BU3>

A;Experimental source: cartilage

A;Note: the first 75 residues of CNBr8, which follows CNBr11

R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
Genomics 4, 438-441, 1989
A>Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide conf
A'Reference number: A30147; MUID:89233138; PMID:2714801
A'Accession: A30147
A'Molecule type: DNA
A'Residues: 104-157, 'P', 159-236 <SUM>
A'CROSS-references: GB:J03065; GB:M23660; GB:M25655; GB:M25730; GB:M32169; GE:
R:Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990
A'Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of pri
A'Reference number: A94227; MUID:90370826; PMID:1975693
A'Accession: A33116
A'Molecule type: DNA
A'Residues: 171-172, 'C', 174-175 <ALA>
A>Note: mutant sequence from a family with primary generalized osteoarthritis
R'Diab, M.; Wu, J.-J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A'Title: Collagen type IX from human cartilage: a structural profile of intermolecular c
A'Reference number: S64673; MUID:96195147; PMID:8660302
A'Accession: S64674
A'Molecule type: protein
A'Residues: 188-189, 'X', 191-195; 1224-1230, 'X', 1232-1236 <DIA>
R'Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage,
Eur. J. Biochem. 234, 125-131, 1995
A'Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cad
A'Reference number: S63514; MUID:96096730; PMID:8529631
A'Accession: S63514
A'Molecule type: Protein
A'Residues: 243-281; 575-590; 756-763, 'X', 765-779 <FRA>
R'Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre,
Am. J. Hum. Genet. 56, 388-395, 1995
A'Title: An RNA-splicing mutation (G->SIVS20) in the type II collagen gene (COL2A1) in a
A'Reference number: I38867; MUID:95150028; PMID:7847372
A'Accession: I38867
A>Status: preliminary; translated from GB/EMBL/DDBJ
A'Molecule type: DNA
A'Residues: 440, 'G', 442-456, 'E', 458-480, 'P', 482-509 <TILA>
A'CROSS-references: EMBL:U15195; NID:g557053; PIDN:AAB60370.1; PID:g557054
R-Ramirez, F.
submitted to the EMBL Data Library, December 1988
A'Reference number: S04892
A'Accession: S04892
A'Molecule type: mRNA
A'Residues: 501-676, 'A', 678-783, 'A', 785-831, 'PA', 834, 'F', 836-1214 <RAM>
A'CROSS-references: EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PID:g930050
R-Vikkuila, M.; Peitonen, L.
FEBS Lett. 250, 171-174, 1989
A'Title: Structural analyses of the polymorphic area in type II collagen gene.
A'Reference number: S05000; MUID:89325561; PMID:2753125
A'Accession: S05000
A'Molecule type: DNA
A'Residues: 630-640, 'A', 642-785 <VIK2>
A'CROSS-references: EMBL:X16159; NID:g29951; PIDN:CAA34278.1; PID:g1335018; PIDN:CAA3427
PIDN:CAA34283.1; PID:g1335023; PIDN:CAA34284.1; PID:g1335024
R-Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D
J. Biol. Chem. 267, 22522-22526, 1992
A'Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro
A'Reference number: A44309; MUID:93054548; PMID:1429602
A'Accession: A44309
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A'Molecule type: DNA; mRNA
A'Residues: 782-831, 'PA', 834, 'F', 836-1005, 'X', 1007-1036, 'Q', 1038-1052, 'E', 1054-1068, 'T',
A'CROSS-references: GB:L00977; NID:g180812; PIDN:AAB23914.1; PID:g258774
A>Note: sequence extracted from NCBI backbone (NCBIPI117273); parts of this sequence wer
A>Note: this translation is not annotated and this publication is not cited in GenBank e
A>Note: mutant sequence associated with perinatal lethal hypochondrogenesis
R-Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990
A'Title: Tandem duplication within a type II collagen gene (COL2A1) exon in an individua
A'Reference number: S16502; MUID:90251662; PMID:2339128
A'Accession: S16502
A'Molecule type: DNA

A:Residues: 1164-1184, 'GPSGKGANGIPGP', 1185-1199 <TIL2>
A:Cross-references: EMBL:M37126, NID:g180808; PIDN:AAA52037.1; PID:g180809
A:Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R:Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
A:Title: Identification and characterization of the human type II collagen gene (COL2A1)
A:Reference number: A02858; MUID:85190534; PMID:3857598
A:Accession: A02858
A:Molecule type: DNA
A:Residues: 1032-1056, 'N', 1058-1068, 'T', 1070-1487 <CHE>
A:Cross-references: GB:J00116; NID:g180395; PIDN:AAA51997.1; PID:g180396
R:Elima, K.; Vuorio, T.; Vuorio, E.
Nucleic Acids Res. 15, 9499-9504, 1987
A:Title: Determination of the single polyadenylation site of the human pro-alpha-1(II)
A:Reference number: A27280; MUID:8806771; PMID:2825137
A:Accession: A27280
A:Molecule type: mRNA
A:Residues: 1175-1487 <ELI>
A:Cross-references: EMBL:X06268; NID:g30096; PIDN:CAA29604.1; PID:g30097
A:Experimental source: fetal epiphyseal cartilage
R:van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 923-925, 1986
A:Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A:Reference number: A57033; MUID:8709927; PMID:3800925
A:Accession: A57033
A:Molecule type: protein
A:Residues: 'XE', 1244-1246, 'N', 1248, 'X', 1250-1265; 1295-1305; 1395-1408 <VAN>
A:Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal pro-
R:Strom, C.M.; Upholt, T.B.
Nucleic Acids Res. 12, 1025-1038, 1984
A:Title: Isolation and characterization of genomic clones corresponding to the human ty-
A:Reference number: A21733; MUID:84118798; PMID:6320112
A:Accession: A21733
A:Molecule type: DNA
A:Residues: 1245-1295 <STR>
A:Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g437897
A:Accession: B21733
A:Molecule type: DNA
A:Residues: 894-909, 'PE', <STR2>
A:Cross-references: GB:X01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
R:Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A:Title: Isolation and partial characterization of genomic clones coding for a human pr
gene.
A:Reference number: A24561; MUID:86104139; PMID:3002437
A:Accession: A24561
A:Molecule type: DNA
A:Residues: 1296-1358 <NUN2>
A:Cross-references: GB:M12048; NID:g180017
A:Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A:Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with th
R:Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Teipouras, P.; Ramirez
Nucleic Acids Res. 13, 2207-2225, 1985
A:Title: Isolation and partial characterization of the entire human pro alpha 1(II) col
A:Reference number: I37249; MUID:85215609; PMID:2987845
A:Accession: S59491
A:Molecule type: DNA
A:Residues: 7-28, 'R', 99-114; 541-578; 786-802; 1055-1056, 'N', 1058-1068, 'T', 1070-1109; 1200-
A:Accession: 184453
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 7-28 <SAN2>
A:Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A:Note: the GenBank PID is based on an incorrect reading frame
A:Accession: I37250
A:Molecule type: DNA
A:Residues: 541-560 <SAN3>
A:Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A:Accession: I37251

Query Match 100.0%; Score 132; DB 1; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;

Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ERGPPGPGQARGFGFTGGLPGVK	23						
Db	265	ERGPPGPGQARGFGFTGGLPGVK	287						
RESULT 5									
A40333									
collagen alpha 1'(II) chain precursor - African clawed frog									
C:Species: Xenopus laevis (African clawed frog)									
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004									
C:Accession: A40333									
R:Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.									
J. Cell Biol. 115, 565-575, 1991									
A:Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis em									
A:Reference number: A40333; MUID:92011898; PMID:1918153									
A:Accession: A40333									
A>Status: nucleic acid sequence not shown									
A:Molecule type: mRNA									
A:Residues: 1-1492 <SUA>									
A:Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596									
A>Note: this sequence is presented as substitutions relative to another sequence in a fil									
es they replace; the appropriate interpretation of the sequence figure was reconstructed									
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology?									
C:Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix									
F:17-96/Domain: von Willebrand factor type C repeat homology <VMC>									
F:1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>									
Query Match 100.0%; Score 132; DB 2; Length 1492;									
Best Local Similarity 100.0%; Pred. No. 1.7e-08;									
- Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ERGPPGPGQARGFGFTGGLPGVK	23						
Db.	270	ERGPPGPGQARGFGFTGGLPGVK	292						
RESULT 6									
A41182									
collagen alpha 1(II) chain precursor - mouse									
C:Species: Mus musculus (house mouse)									
C>Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999									
C:Accession: A41182; A44885									
R:Metzger, M.; Toman, D.; de Crombrughe, B.; Vuorio, E.									
J. Biol. Chem. 266, 16862-16869, 1991									
A:Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and									
A:Reference number: A41182; MUID:91358489; PMID:1885613									
A:Accession: A41182									
A>Status: preliminary; not compared with conceptual translation									
A:Molecule type: DNA									
A:Residues: 1-1419 <MET>									
A:Cross-references: GB:M65161									
R:Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.									
Development 111, 945-953, 1991									
A:Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilag									
A:Reference number: A44885; MUID:91347939; PMID:1879363									
A:Accession: A44885									
A:Molecule type: DNA									
A:Residues: 1-128 <CHE>									
A:Cross-references: GB:S63190; NID:g234368; PIDN:AAB19627.1; PID:g234369									
A>Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBI:63192)									
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology?									
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime									
F:1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>									
Query Match 92.4%; Score 122; DB 2; Length 1419;									
Best Local Similarity 95.7%; Pred. No. 2.7e-07;									
Matches	22;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	ERGPPGPGQARGFGFTGGLPGVK	23						
Db	197	ERGPPGPGQARGFGFTGGLPGVK	219						

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;5/Modified site: allylsine (Lys) #status predicted
 F;21,27,36,39,42,54,57,66,72,87,90,93,111,114,120,123,129,138,147,174,177,180,192,207,211
 xperimental
 F;66,111/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F;96,117,132,183/Modified site: 5-hydroxylysine (Lys) #status experimental
 F;228,273/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 89.4%; Score 118; DB 1; Length 402;
 Best Local Similarity 91.3%; Pred. No. 2.5e-07;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPFGTGLPGVK 23
 |||||
 Db 74 ERGVPGPGARGPFGTGLPGFK 96
 |||||

RESULT 9
 CGB01S
 collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 24-Apr-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
 C;Accession: A91193; A91229; A91387; A91211; A91201; A91200; A43048; A02853
 R;Rautenberg, J.; Timpl, R.; Furchmayr, H.
 Eur. J. Biochem. 27, 231-237, 1972

A;Title: Structural characterization of N-terminal antigenic determinants in calf and hu
 A;Reference number: A91193; MUID:72255334; PMID:4115172
 A;Accession: A91193
 A;Molecule type: protein
 A;Residues: 1-19 <RAU>
 A;Cross-references: UNIPROT:P02453
 A;Experimental source: skin
 A;Note: The epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is conve
 R;Fietzek, P.P.; Kuehn, K.
 Eur. J. Biochem. 52, 77-82, 1975

A;Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide
 A;Reference number: A91229; MUID:76022320; PMID:1164916
 A;Accession: A91229
 A;Molecule type: protein
 A;Residues: 20-145 <FIE>
 A;Experimental source: skin
 A;Note: Lys-103 is hydroxylated and binds glucosylgalactose
 R;Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
 FEBS Lett. 26, 74-76, 1972

A;Title: The covalent structure of collagen: amino acid sequence of alpha1-CB3 from calf
 A;Reference number: A91387; MUID:73049499; PMID:4673951
 A;Accession: A91387
 A;Molecule type: protein
 A;Residues: 146-294 <F12>
 A;Experimental source: skin
 R;Fietzek, P.P.; Rextrodt, F.W.; Hopper, K.E.; Kuehn, K.
 Eur. J. Biochem. 38, 396-400, 1973

A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alpha1-CB7 fr
 A;Reference number: A91211; MUID:74086118; PMID:4359390
 A;Accession: A91211
 A;Molecule type: protein
 A;Residues: 295-562 <F13>
 A;Experimental source: skin
 R;Wendt, P.; Mark, K.V.D.; Rextrodt, F.; Kuehn, K.
 Eur. J. Biochem. 30, 169-183, 1972

A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues
 A;Reference number: A91201; MUID:73042276; PMID:4343808
 A;Accession: A91201
 A;Molecule type: protein
 A;Residues: 563-675 <WEN>
 A;Experimental source: skin
 R;Fietzek, P.P.; Rextrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
 Eur. J. Biochem. 30, 163-168, 1972

A;Title: The covalent structure of collagen. Amino acid sequence of peptide alpha1-CB6-C
 A;Reference number: A91200; MUID:73042275; PMID:4343807
 A;Accession: A91200
 A;Molecule type: protein
 A;Residues: 676-758 <F14>

A;Experimental source: skin
 A;Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in posit
 R;Rautenberg, J.; Fietzek, P.; Rextrodt, F.; Becker, U.; Stark, M.; Kuehn, K.
 FEBS Lett. 21, 75-79, 1972

A;Title: The amino acid sequence of the carboxyterminal nonhelical cross link region of
 A;Reference number: A43048
 A;Accession: A43048
 A;Molecule type: protein
 A;Residues: 759-779 <RA2>
 A;Experimental source: skin
 C;Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydro
 C;Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are
 C;Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin
 9, 149, 268, and 217 residues.
 C;Comment: The complete chain contains 1052 residues.
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer;
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 87.1%; Score 115; DB 1; Length 779;
 Best Local Similarity 87.0%; Pred. No. 1.1e-06;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPFGTGLPGVK 23
 |||||
 Db 81 ERGPPGPGARGPFGTGLPGMK 103
 |||||

RESULT 10
 S21626
 collagen alpha 1(I) chain precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence revision 25-Apr-1997 #text change 09-Jul-2004
 C;Accession: S57243; S16374; A23982; I49559; S39789; I48300; S21626
 R;Li, S.W.; Khillan, J.; Prockop, D.J.
 Matrix Biol. 14, 593-595, 1994

A;Title: The complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of type I
 A;Reference number: S57243
 A;Accession: S57243
 A;Molecule type: mRNA
 A;Residues: 1-1453 <LIS>
 A;Cross-references: UNIPROT:P11087; EMBL:U08020; NID:G470673; PIDN:AAA88912.1; PID:G470
 R;Metsaeranta, M.; Toman, D.; de Crombrughe, B.; Vuorio, E.
 Biochim. Biophys. Acta 1089, 241-243, 1991

A;Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.
 A;Reference number: S16176; MUID:91274355; PMID:2054384
 A;Accession: S16374
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1442-1453 <MET>
 A;Cross-references: EMBL:X57981; NID:G50484; PIDN:CAA41046.1; PID:G50485
 R;French, B.T.; Lee, W.H.; Maul, G.G.
 Gene 39, 311-312, 1985

A;Title: Nucleotide sequence of a cDNA clone for mouse proalpha1(I) collagen protein.
 A;Reference number: A23982; MUID:86137403; PMID:3841523
 A;Accession: A23982
 A;Molecule type: mRNA
 A;Residues: 518-1128 <PRE>
 A;Cross-references: GB:M14423; NID:G192261; PIDN:AAA37333.1; PID:G192262
 R;Monson, J.M.; Friedman, J.; McCarthy, B.J.
 Mol. Cell. Biol. 2, 1362-1371, 1982

A;Title: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for
 A;Reference number: I49559; MUID:83141374; PMID:6298597
 A;Accession: I49559
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 735-1130 <RES>
 A;Cross-references: GB:M17491; NID:G192263; PIDN:AAA37334.1; PID:G192264
 R;Harbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
 Proc. Natl. Acad. Sci. U.S.A. 81, 1504-1508, 1984

A;Title: Insertion of retrovirus into the first intron of alpha1(I) collagen gene leads
 A;Reference number: I49557; MUID:84170331; PMID:6324198
 A;Accession: I49557

A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-25 <RE2>
A:CROSS-references: GB:K01688; NID:gl92246; PIDN:AAA37330.1; PID:g553881
R:Fonton, S.F.; Lamané, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.P.
Biochim. Biophys. Acta 1216, 469-474, 1993
A>Title: Genomic sequence of mouse COL1A1 encoding the collagen propeptides.
A:Reference number: S39789; MUID:94092741; PMID:8268229
A:Accession: S39789
A:Molecule type: DNA
A:Residues: 1-80, 'E', 82-105, 'D', 107-185, 1031-1201, 'G', 1203-1218, 'E', 1220-1221, 'T', 1223-1
R:Rhodes, K.; Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Mol. Cell. Biol. 14, 5950-5960, 1994
A>Title: DNA methylation represses the murine alpha 1(I) collagen promoter by an indirect
A:Reference number: I48300; MUID:94344105; PMID:8065328
A:Accession: I48300
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-80, 'E', 82-105, 'D', 107-147 <REF>
A:CROSS-references: EMBL:X54876; NID:g50486; PIDN:CRA38657.1; PID:g50487
C:Genetics:
A:Gene: COL1A1
A:Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 932/3; 968/3; 1004/3; 1022/3; 1058/
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; triple helix
F:1-22/Domain: signal sequence #status predicted <SIG>
F:33-151/Domain: amino-terminal propeptide #status predicted <PRO>
F:30-89/Domain: von Willebrand factor type C repeat homology <VWC>
F:152-1453/Product: collagen alpha 1(I) chain #status predicted <VAT>
F:1224-1453/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
Query Match 87.1%; Score 115; DB 2; Length 1453;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy* 1 ERGPPGPGQARGFGPTGLPGVK 23
|||||
Db 232 ERGPPGPGQARGFGPTGLPGMK 254
|||||
RESULT 11
CGHUI5
collagen alpha 1(I) chain precursor - human
N:Alternate names: procollagen alpha 1(I) chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 09-Jul-2004
C:Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11
5269; A29439; I53466; A02852; I37247
R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.
Gene 67, 105-115, 1988
A>Title: Complete nucleotide sequence of the region encompassing the first twenty-five e
A:Reference number: I60114; MUID:88329734; PMID:2843432
A:Accession: I60114
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-369, 'L', 371-589 <DAL>
A:CROSS-references: UNIPROT:P02452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNIF
R:Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock
Biochem. J. 253, 919-922, 1988
A>Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
A:Reference number: S01143; MUID:89025644; PMID:3178743
A:Accession: S01143
A:Molecule type: mRNA
A:Residues: 1-472 <TRO>
A:CROSS-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M3546; NID
A>Note: submitted to the EMBL/GenBank/DBJ databases by Prockop, D.J., 13-JUN-1988
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Nature 310, 337-340, 1984
A>Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of
A:Reference number: A93335; MUID:84270697; PMID:6462220
A:Accession: A93335
A:Molecule type: DNA
A:Residues: 1-58, 'Q', 60-181 <CHU>

A:CROSS-references: EMBL:X00820; NID:g35657; PIDN:CNA25394.1; PID:g35658
R:Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.
J. Biol. Chem. 262, 15151-15157, 1987
A>Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh
A:Reference number: I55254; MUID:88033098; PMID:2822714
A:Accession: I55254
A>Status: translation not shown; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-45 <ROS>
A:CROSS-references: GB:J02829; NID:gl80387; PIDN:AAA51993.1; PID:gl80388
R:Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gellinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A>Title: Regulatory elements in the first intron contribute to transcriptional control o
A:Reference number: A39943; MUID:88097389; PMID:3480516
A:Accession: A39943
A:Molecule type: DNA
A:Residues: 1-34 <BOR>
A:CROSS-references: GB:J03559; NID:gl80876; PIDN:AAA52052.1; PID:g553238
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A>Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter s
A:Reference number: I55237; MUID:85130970; PMID:2857713
A:Accession: I55237
A>Status: translation not shown; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-34 <CH2>
A:CROSS-references: GB:M10627; NID:gl80383; PIDN:AAA51992.1; PID:g553226
R:Wittz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
J. Biol. Chem. 265, 6312-6317, 1990
A>Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina
rome, type VII.
A:Reference number: A35233; MUID:90202908; PMID:2318855
A:Accession: A35233
A:Molecule type: protein
A:Residues: 33-52 <WIR>
A>Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
R:Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
EMBO J. 8, 1705-1710, 1989
A>Title: A base substitution in the exon of a collagen gene causes alternative splicing
A:Reference number: S09400; MUID:89356643; PMID:2767050
A:Accession: S09400
A:Molecule type: mRNA
A:Residues: 156-183 <WEI>
R:Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A>Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
A:Reference number: A30567; MUID:71038625; PMID:5529814
A:Contents: CNB0-1, CNB2, CNB4, CNB5
A:Accession: B90567
A:Molecule type: protein
A:Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z',
A:Experimental source: skin
A>Note: evidence for 170-allysine
R:Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P.
Eur. J. Biochem. 192, 153-159, 1990
A>Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle
A:Reference number: S11372; MUID:90382436; PMID:2169412
A:Accession: S11372
A:Molecule type: protein
A:Residues: 175-187, 274-287, 'P', 289 <BAE>
A>Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R:Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
J. Biol. Chem. 266, 21827-21832, 1991
A>Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
operative melting of intact type I collagen.
A:Reference number: I55342; MUID:92042092; PMID:1718984
A:Accession: I55342
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 258-268, 1347-1357 <DEA>
A:CROSS-references: GB:S67495; NID:g239007; PIDN:AAB20350.1; PID:g239008
A>Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R:Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.

J. Biol. Chem. 245, 5042-5048, 1970
A:Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A:Reference number: A92069; MUID:71001508; PMID:4319110
A:Accession: A92069
A:Molecule type: protein
A:Residues: 263-268 <MOR>
A:Experimental source: skin
A:Note: Attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
R:Labhard, M.E.; Hollister, D.W.
Matrix 10, 124-130, 1990
A:Title: Segmental amplification of the entire helical and telopeptide regions of the ch
A:Reference number: S15989; MUID:90326017; PMID:2374517
A:Accession: S15989
A:Molecule type: mRNA
A:Residues: 281-302
R:Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N
Connect. Tissue Res. 29, 1-11, 1993
A:Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A:Reference number: I52905; MUID:93339042; PMID:8339541
A:Accession: I52905
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 342-352, 'C', 354-359 <W2>
A:Cross-references: GB:S64717; NID:9408195; PIDN:AAB27677.1; PID:9408196
A:Note: Mutant sequence from patient with osteogenesis imperfecta
R:Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-5223, 1983
A:Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha
A:Reference number: A90476; MUID:84080385; PMID:6689127
A:Accession: A90476
A:Molecule type: mRNA
A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>
A:Cross-references: GB:K01228; NID:G180391; PIDN:AAA51995.1; PID:G180392
A:Note: sequence partially completed for missing nucleotides by A29439
R:Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A:Title: Multixon deletion in an osteogenesis imperfecta variant with increased type II
A:Reference number: A22161; MUID:85104934; PMID:2981843
A:Accession: A22161
A:Molecule type: DNA
A:Residues: 472-594, 'R', 596-607 <H3>
A:Cross-references: GB:K03178; GB:K03179; NID:G179612; NID:G179613; PIDN:AAA51847.1; PID
A:Note: the authors translated the codon CGT for residue 595 as Pro
R:Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A:Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
A:Reference number: A35336; MUID:90252792; PMID:2339700
A:Accession: A35336
A:Molecule type: mRNA
A:Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
A:Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R:Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Motte
Hum. Mol. Genet. 3, 2201-2206, 1994
A:Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the c
A:Reference number: I54365; MUID:95187161; PMID:7881420
A:Accession: I54365
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 746-766, 'S', 768-781 <FOR>
A:Cross-references: GB:L47667; NID:G1009093; PIDN:AAB59576.1; PID:G1009094
R:Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A:Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
A:Reference number: A47426; MUID:93352646; PMID:8349697
A:Accession: A47426
A:Molecule type: mRNA
A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>
A:Cross-references: GB:S64596; NID:G407589; PIDN:AAB27856.1; PID:G407590
A:Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIPI:136445)
A:Note: does not represent an experimentally determined sequence but three different mut
A:Accession: B47426
A:Molecule type: mRNA

A:Residues: 1179-1464 <CH4>
A:Experimental source: normal dermal fibroblast culture
A:Accession: C47426
A:Molecule type: mRNA
A:Residues: 1179-1276, 'H', 1278-1464 <CH5>
A:Experimental source: fetal cell 86-237
A:Accession: D47426
A:Molecule type: mRNA
A:Residues: 1179-1336, 1339-1464 <CH6>
A:Experimental source: fetal cell 86-146
A:Accession: E47426
A:Molecule type: mRNA
A:Residues: 1179-1387, 'R', 1389-1464 <CH7>
A:Experimental source: fetal cell 88-251
R:Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; N
J. Biol. Chem. 263, 14605-14607, 1988
A:Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide
A:Reference number: I55269; MUID:89008319; PMID:3170557
A:Accession: I55269
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1187-1194, 'C', 1196-1220 <COH>
A:Cross-references: GB:M23213; NID:9340842; PIDN:AAB59363.1; PID:G499622
A:Note: Mutant sequence from a patient with mild osteogenesis imperfecta
R:Mackelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A:Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
Query Match 87.1%; Score 115; DB 1; Length 1464;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ERGPPGPGQARGFPFGTGLPGVK 23
DB 243 ERGPPGPGQARGLPGTAGLPGMK 265
RESULT 12
A05249
collagen alpha 1(I) chain precursor - baboon (tentative sequence) (fragment)
C:Species: Papio sp. (baboon)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05249
R:Epstein Jr., E.H.; Scott, R.D.; Miller, E.J.; Piez, K.A.
J. Biol. Chem. 246, 1718-1724, 1971
A:Title: Isolation and characterization of the peptides derived from soluble human and
A:Reference number: A92078; MUID:71134791; PMID:4993958
A:Contents: CNBr0-1, CNBr2, CNBr4, CNBr5, composition
A:Accession: A05249
A:Molecule type: protein
A:Residues: 1-140 <EPS>
A:Cross-references: UNIPROT:Q7M2V1
A:Experimental source: skin
C:Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are i
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; skin; trimer; triple helix
Query Match 84.8%; Score 112; DB 2; Length 140;
Best Local Similarity 78.3%; Pred. No. 5.1e-07;
Matches 18; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 ERGPPGPGQARGFPFGTGLPGVK 23
DB 82 ZRGPPGPGARGLPGTAGLPGMK 104
RESULT 13
CGRT15
collagen alpha 1(I) chain - rat (tentative sequence) (fragments)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
C:Accession: A90559; A90552; A92029; A90353; A90566; A90362; A90379; A91209; A9
R:Bornstein, P.

Biochemistry 8, 63-71, 1969
A:Title: Comparative sequence studies of rat skin and tendon collagen. II. The absence of
A:Reference number: A90559; MUID:69155173; PMID:5777344
A:Contents: CNBx0 and CNBx1
A:Accession: A90559
A:Molecule type: protein
A:Residues: 1-19 <BOL>
A:Experimental source: tendon
A:Note: sequences from skin and tendon appear to be identical
R:Kang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A:Title: The amino acid sequence of peptides from the cross-linking region of rat skin c
A:Reference number: A90552; MUID:67162268; PMID:5337886
A:Contents: CNBx1
A:Accession: A90552
A:Molecule type: protein
A:Residues: 5-19 <KAN>
A:Experimental source: skin
R:Bornstein, P.
J. Biol. Chem. 242, 2572-2574, 1967
A:Title: The incomplete hydroxylation of individual prolyl residues in collagen.
A:Reference number: A92029; MUID:67165368; PMID:4290711
A:Contents: CNBx2
A:Accession: A92029
A:Molecule type: protein
A:Residues: 20-55 <BO2>
A:Experimental source: skin and tendon
R:Butler, W.T.; Ponder, S.L.
Biochemistry 10, 2076-2081, 1971
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a
A:Reference number: A90353; MUID:71263178; PMID:4327399
A:Contents: CNBx4
A:Accession: A90353
A:Molecule type: protein
A:Residues: 56-102 <BU1>
A:Experimental source: skin
R:Butler, W.T.
Biochemistry 9, 44-50, 1970
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The cov
A:Reference number: A90566; MUID:70085124; PMID:5411206
A:Contents: CNBx5
A:Accession: A90566
A:Molecule type: protein
A:Residues: 103-139 <BU2>
A:Experimental source: skin
R:Ballan, G.; Click, E.M.; Bornstein, P.
Biochemistry 10, 4470-4478, 1971
A:Title: Structure of rat skin collagen alphas 1(I)-C88. Amino acid sequence of the hydroxyla
A:Reference number: A90357; MUID:72136131; PMID:4335087
A:Contents: CNBx8
A:Accession: A90357
A:Molecule type: protein
A:Residues: 140-238 <BA1>
A:Experimental source: skin
R:Ballan, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P.
Biochemistry 11, 3798-3806, 1972
A:Title: Structure of rat skin collagen alphas 1(I)-C88. Amino acid sequence of the hydroxyla
A:Reference number: A90362; MUID:73006942; PMID:4342027
A:Contents: CNBx8
A:Accession: A90362
A:Molecule type: protein
A:Residues: 239-418 <BA2>
A:Experimental source: skin
R:Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
Biochemistry 13, 2946-2953, 1974
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a
A:Reference number: A90379; MUID:74271984; PMID:4366532
A:Contents: CNBx3
A:Accession: A90379
A:Molecule type: protein
A:Residues: 419-567 <BU3>
A:Experimental source: skin

R:Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 37, 287-294, 1973
A:Title: Structural and immunogenic properties of a major antigenic determinant in neutr
A:Reference number: A91209; MUID:74011954; PMID:4126850
A:Contents: CNBx6
A:Accession: A91209
A:Molecule type: protein
A:Residues: 568-651 <ST1>
A:Experimental source: skin
A:Note: this region probably corresponds to positions 949-1032 of the alpha 1(I) chain
A:Note: the major antigenic determinant (of neutral salt-extracted rat skin collagen) in
R:Stoltz, M.; Timpl, R.; Kuehn, K.
FEBS Lett. 26, 61-65, 1972
A:Title: Non-helical regions in rat collagen alpha-chain.
A:Reference number: A91385; MUID:73049495; PMID:4636751
A:Contents: CNBx6
A:Accession: A91385
A:Molecule type: protein
A:Residues: 651-671 <ST2>
A:Experimental source: skin
A:Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequen
A:Note: this region (residues 651-671 above) probably corresponds to positions 1032-1052
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Comment: The order of the nine CNBR peptides in the alpha 1(I) chain of rat skin colla
C:Comment: The complete chain contains 1052 residues.
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: blocked amino end; coiled coil; extracellular matrix; glycoprotein; hydroxyl
F:1/Modified site: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #statu
F:9/Modified site: allylsine (Lys) #status experimental
F:103,424,547/Binding site: carboxylate (Lys) (covalent) #status experimental
F:103/Modified site: 5-hydroxylysine (Lys) #status experimental
F:424,547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 84.8%; Score 112; DB 1; Length 671;
Best Local Similarity 82.6%; Pred. No. 2.2e-06;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPGPGQARGFPPTGLPGVK 23
:|||||:|||||:|||||:|
Db 81 QRGPFGPGQARGLPGTGLPGMK 103

RESULT 14
CGCH1S
collagen alpha 1(I) chain - chicken (tentative sequence) (fragments)
C:Species: Gallus gallus (chicken)
C>Date: 12-Aug-1981 #sequence revision 06-Jul-1982 #text_change 31-Mar-2000
C:Accession: A90458; A90181; A02857
R:Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J
Biochemistry 21, 2048-2055, 1982
A:Title: Amino acid sequence of chick skin collagen alpha 1(I)-C88 and the complete prim
A:Reference number: A90458; MUID:82231995; PMID:7093229
A:Accession: A90458
A:Molecule type: protein
A:Residues: 1-1036 <HIC>
A:Experimental source: skin
A:Note: this is the latest in a series of papers from these workers elucidating the seq
R:Eyre, D.R.; Glimcher, M.J.
Biochem. Biophys. Res. Commun. 48, 720-726, 1972
A:Title: Evidence for a previously undetected sequence at the carboxyterminus of the al
A:Reference number: A90181; MUID:72243016; PMID:5047697
A:Accession: A90181
A:Molecule type: protein
A:Residues: 1037-1042 <EYR>
A:Experimental source: skin
A:Note: residues 1037-1042 above correspond to the carboxyl end of the protein
C:Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in som
C:Comment: Most of the prolines at the third position of the tripeptide repeating unit
C:Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in p
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: coiled coil; extracellular matrix; glycoprotein; pyrrolidone carboxylic acid; trimer;
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 84.8%; Score 112; DB 1; Length 1042;
 Best Local Similarity 82.6%; Pred. No. 3, 4e-06;
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPPGQAGFGPTGGLGVK 23
 :||||||| ||| |||||
 Db 81 QRGPPPGQAGFLGTAGLGMK 103

RESULT 15
 collagen alpha 2(I) chain precursor - human
 N;Alternate names: procollagen alpha 2(I) chain
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1989 #sequence revision 25-Aug-1995 #text change 09-Jul-2004
 C;Accession: A28500; S00824; S09176; I55311; A58111; A28472; A42165; A34405; A90567; I55305; A02865
 R;de Wet, W.; Bernard, M.; Benson-Chanda, V.; Chu, M.L.; Dickson, L.; Weil, D.; Ramirez, J. Biol. Chem. 262, 16032-16036, 1987
 A;Title: Organization of the human pro-alpha-2(I) collagen gene.
 A;Reference number: A28500; MUID:88058962; PMID:2824475
 A;Accession: A28500
 A;Molecule type: DNA; mRNA
 A;Residues: 1-248,'N',250-1366 <DEW>
 A;Cross-references: UNIPROT:P08123; UNIPROT:Q14038; UNIPROT:Q9UM83; UNIPROT:Q9UNM6; UNIPROT:Q9UNM7
 R;Kuivaniemi, H.; Tromp, G.; Chu, M.L.; Prockop, D.J.
 Biochem. J. 252, 633-640, 1988
 A;Title: Structure of a full-length cDNA clone for the prepro-alpha-2(I) chain of human
 A;Reference number: S00824; MUID:88339824; PMID:3421913
 A;Accession: S00824
 A;Molecule type: mRNA
 A;Residues: 1-275,'A',277-332,'V',334-337,'A',339-482,'A',484-548,'D',550-765 <KU11>
 A;Cross-references: EMBL:Y00724; NID:G30022; PIDN:CAA68709.1; PID:G30023
 R;Dickson, L.A.; de Wet, W.; di Liberto, M.; Weil, D.; Ramirez, F.
 Nucleic Acids Res. 13, 3427-3438, 1985
 A;Title: Analysis of the promoter region and the N-propeptide domain of the human proalpha-2(I) chain of collagen
 A;Reference number: S09176; MUID:85242047; PMID:4011429
 A;Accession: S09176
 A;Molecule type: DNA
 A;Residues: 1-237,33-58,'P',60-93 <DIC>
 A;Cross-references: EMBL:X02498; NID:G30098; PIDN:CAA26320.1; PID:G30099
 R;Weil, D.; D'Alessio, M.; Ramirez, F.; Eyre, D.R.
 J. Biol. Chem. 265, 16007-16011, 1990
 A;Title: Structural and functional characterization of a splicing mutation in the pro-alpha-2(I) chain of collagen
 A;Reference number: I55311; MUID:90368825; PMID:2394758
 A;Accession: I55311
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 76-93 <WE11>
 A;Cross-references: GB:M35391; NID:G189684; PIDN:AAA60041.1; PID:G189685
 A;Accession: A58111
 A;Molecule type: protein
 A;Residues: 23-75,94-96 <WE12>
 A;Note: mutant sequence from a patient with Ehlers-Danlos syndrome type VII
 R;Wirtz, M.K.; Gnanville, R.W.; Steinmann, B.; Rao, V.H.; Hollister, D.W.
 J. Biol. Chem. 262, 16375-16385, 1987
 A;Title: Ehlers-Danlos syndrome type VII. Deletion of 18 amino acids comprising the N-terminal propeptide
 A;Reference number: A28472; MUID:88059013; PMID:3680255
 A;Accession: A28472
 A;Molecule type: protein
 A;Residues: 32-75,94-111 <WIR>
 A;Note: mutant sequence of patient with Ehlers-Danlos syndrome type VII
 R;Chiodo, A.A.; Hockley, A.; Cole, W.G.
 J. Biol. Chem. 267, 6361-6369, 1992
 A;Title: A base substitution at the splice acceptor site of intron 5 of the COL1A2 gene
 s-Danlos syndrome type VII.
 A;Reference number: A42165; MUID:92210617; PMID:1556139
 A;Accession: A42165
 A;Molecule type: mRNA
 A;Residues: 50-126 <CHI>
 A;Note: parts of this sequence were determined by protein sequencing; a mutant sequence
 R;Weil, D.; D'Alessio, M.; Ramirez, F.; Steinmann, B.; Wirtz, M.K.; Gnanville, R.W.; Hollister, D.W.

J. Biol. Chem. 264, 16804-16809, 1989
 A;Title: Temperature-dependent expression of a collagen splicing defect in the fibroblast
 A;Reference number: A34405; MUID:89380311; PMID:2777808
 A;Accession: A34405
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 58-108 <WE13>
 A;Cross-references: GB:J05049
 A;Note: the accession cited by the authors is not found in GenBank
 A;Note: parts of this sequence were determined by protein sequencing; a mutant having 9
 R;Click, E.M.; Bornstein, P.
 Biochemistry 9, 4699-4706, 1970
 A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
 A;Reference number: A90567; MUID:71038625; PMID:5529814
 A;Accession: A90567
 A;Molecule type: protein
 A;Residues: 'Z',81,'B',83-96;417-447 <CLI>
 A;Note: the compositions of peptides CNBr1, CNBr0, and CNBr2 were determined; evidence
 R;Kuivaniemi, H.; Sabol, C.; Tromp, G.; Sippola-Thiele, M.; Prockop, D.J.
 J. Biol. Chem. 263, 11407-11413, 1988
 A;Title: A 19-base pair deletion in the pro-alpha 2(I) gene of type I procollagen that
 is asymptomatic mother
 A;Reference number: I55264; MUID:88298792; PMID:3403536
 A;Accession: I55264
 A;Status: translation not shown; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA; mRNA
 A;Residues: 145-197 <KUI2>
 A;Cross-references: GB:M21671; NID:G189521; PIDN:AAA59994.1; PID:G553606
 A;Note: single base mutation in intron leads to abnormal splicing of mRNA
 R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W.
 J. Bone Miner. Res. 7, 793-805, 1992
 A;Title: Expression of mutant alpha (I)-procollagen in osteoblast and fibroblast cultur
 A;Reference number: I55485; MUID:92351816; PMID:1642148
 A;Accession: I55485
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 163-181,200-213 <CH2>
 A;Cross-references: GB:S41099; NID:G252702; PIDN:AAB22761.1; PID:G252703
 A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
 R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
 J. Biol. Chem. 245, 5042-5048, 1970
 A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
 A;Reference number: A92069; MUID:71001508; PMID:4319110
 A;Accession: B92069
 A;Molecule type: protein
 A;Residues: 175-180 <MOR>
 A;Experimental source: skin
 A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
 R;Fietzek, P.P.; Furthmayr, H.; Kuehn, K.
 Eur. J. Biochem. 47, 257-261, 1974
 A;Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-sk
 A;Reference number: A91224; MUID:75008198; PMID:4412529
 A;Accession: A91224
 A;Molecule type: protein
 A;Residues: 418-447 <FIE>
 R;Tromp, G.; Prockop, D.J.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5254-5258, 1988
 A;Title: Single base mutation in the pro alpha 2(I) collagen gene that causes efficient
 A;Reference number: I59125; MUID:88276936; PMID:2839839
 A;Accession: I59125
 A;Status: translation not shown; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 520-573 <TRO>
 A;Cross-references: GB:M21353; NID:G180881; PIDN:AAA52053.1; PID:G180882
 A;Note: single base mutation in intron leads to splicing out of exon 28
 R;Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
 Biochemistry 22, 1139-1145, 1983
 A;Title: Structure of a cDNA for the proalpha-2 chain of human type I procollagen. Comp
 A;Reference number: S09174; MUID:83178919; PMID:6687691
 A;Accession: S09174
 A;Molecule type: mRNA
 A;Residues: 623-742,'A',744-764,'X',766-827,'A',829-830,'P',832-836,'P',838-1097,'L',10

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Query Match      82.6%;   Score 109;   DB 1;   Length 1366;
Best Local Similarity 87.0%;   Pred. No. 1e-05;
Matches 20;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy      1  ERGPPPGQARGPFGTGLPGVK 23
      |||  |||  |||  |||  |||  |||  |||
Db      155 ERGVVPGQARGPFGTGLPGFK 177

Search completed: October 8, 2005, 00:27:22
Job time : 39 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 00:04:32 ; Search time 176 Seconds
(without alignments)
66.919 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132
Sequence: 1 ERGPPGPGARGFGTGLPGVK 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	243	Q14045	Q14045 homo sapien
2	132	100.0	747	CA12_BOVIN	P02459 bos taurus
3	132	100.0	1160	Q14046	Q14046 homo sapien
4	132	100.0	1269	Q7T227	Q7T227 gallus gall
5	132	100.0	1418	CA12_HUMAN	Q28458 homo sapien
6	132	100.0	1418	Q28396	Q28396 equus caball
7	132	100.0	1418	Q9W7R9	Q9W7R9 cynops pyrr
8	132	100.0	1420	Q90W37	Q90W37 gallus gall
9	132	100.0	1486	Q91717	Q91717 xenopus lae
10	132	100.0	1486	Q7ZTI6	Q7ZTI6 xenopus lae
11	132	100.0	1487	Q14047	Q14047 homo sapien
12	132	100.0	1487	Q77753	Q77753 canis famil
13	132	100.0	1491	Q91718	Q91718 xenopus lae
14	132	100.0	1491	Q7ZTM4	Q7ZTM4 xenopus lae
15	132	100.0	1492	Q6P4Z2	Q6P4Z2 xenopus tiro
16	131	99.2	1447	Q6P4U1	Q6P4U1 brachydanio
17	131	99.2	1447	Q6U1J5	Q6U1J5 brachydanio
18	132	92.4	1419	Q63123	Q63123 rattus norv
19	132	92.4	1419	Q80VY3	Q80VY3 mus musculu
20	132	92.4	1419	Q80X38	Q80X38 mus musculu
21	132	92.4	1487	Q641K3	Q641K3 mus musculu
22	118	89.4	1355	CA12_RANCA	Q42350 rana catesb
23	117	88.6	1442	Q62031	Q62031 mus musculu
24	117	88.6	1442	Q62033	Q62033 mus musculu
25	117	88.6	1459	CA12_MOUSE	P28481 mus musculu
26	117	88.6	1459	Q62032	Q62032 mus musculu
27	115	87.1	187	Q9BDZ2	Q9BDZ2 macaca mul
28	115	87.1	343	Q46388	Q46388 equus caball
29	115	87.1	779	CA11_BOVIN	P02453 bos taurus
30	115	87.1	1069	Q6LAN8	Q6LAN8 homo sapien
31	115	87.1	1225	Q6PCL3	Q6PCL3 mus musculu

RESULT 1

Q14045 PRELIMINARY; PRT; 243 AA.
AC Q14045;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Collagen II alpha 1 chain (Fragment).
GN Name-COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal sternum;
RX MEDLINE=91153296; PubMed=1999183;
RA Huang M.C., Seyer J.M., Thompson J.P., Spinella D.G., Cheah K.S.,
RA Kang A.H.;
RT "Genomic organization of the human procollagen alpha 1(II) collagen
RT gene.";
RL Eur. J. Biochem. 195:593-600(1991).
DR EMBL; X57010; CAA40330.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 4.
DR ProDom; PD000007; Clg_helix; 1.
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 22697 MW; 021130504652F69B CRC64;

Query Match 100.0%; Score 132; DB 2; Length 243;

Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGFGTGLPGVK 23

DB 167 ERGPPGPGARGFGTGLPGVK 189

RESULT 2

CA12_BOVIN STANDARD; PRT; 747 AA.
AC P02459; Q28070; Q9XT24;
DT 21-JUL-1986 (Rel. 01, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Collagen alpha 1(II) chain precursor (Fragments).
GN Name-COL2A1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC

ID Q14046 PRELIMINARY; PRT; 1160 AA.
AC Q14046;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE COL2A1 protein precursor (Fragment).
GN Name=COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=90026318; PubMed=2803268;
RA Baldwin C.T., Reginato A.M., Smith C., Jimenez S.A., Prockop D.J.;
RT "Structure of cDNA clones coding for human type II procollagen. The
RT alpha 1(II) chain is more similar to the alpha 1(I) chain than two
RT other alpha chains of fibrillar collagens.";
RL Biochem. J. 262:521-528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Prockop D., Baldwin C.T., Reginato A.M., Smith C., Jimenez S.;
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X16711; CAA34683.1; -;
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:000817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 18.
DR- ProbDom; PD000007; Clg helix; 6.
KW Collagen; Matrix protein; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 113 >1160 collagen.
FT NON_TER 1160 1160
SQ SEQUENCE 1160 AA; 105630 MW; A7F0523B856C8639 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1160;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGTGLPGVK 23
Db 196 ERGPPGPGQARGFGTGLPGVK 218

RESULT 4
Q7T2Z7 PRELIMINARY; PRT; 1269 AA.
AC Q7T2Z7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1 type II procollagen (Fragment).
GN Name=COL2A1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Caixia X., Yongzhi X., Siqi G., Yuying S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452711; AAO33039.2; -;
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.

DR InterPro; IPR000895; Fib.collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 17.
DR ProbDom; PD000007; Clg helix; 6.
DR ProbDom; PD002078; Fib.collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Collagen.
FT NON_TER 1
SQ SEQUENCE 1269 AA; 120116 MW; 446EF91BEB8BF6A CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGTGLPGVK 23
Db 47 ERGPPGPGQARGFGTGLPGVK 69

RESULT 5
CA12_HUMAN STANDARD; PRT; 1418 AA.
ID CA12_HUMAN
AC P02458;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin].
GN Name=COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90067946; PubMed=2597267;
RA Su M.W., Lee B., Ramirez F., Machado M.A., Horton W.A.;
RT "Nucleotide sequence of the full length cDNA encoding for human type
RT II procollagen.";
RL Nucleic Acids Res. 17:9473-9473(1989).
RN [2]
RP SEQUENCE OF 1-28 FROM N.A., AND VARIANT THR-9.
RX MEDLINE=87031574; PubMed=3021582; DOI=10.1016/0378-1119(86)90037-5;
RA Nunez A.M., Kohno K., Martin G.R., Yamada Y.;
RT "Promoter region of the human pro-alpha 1(II)-collagen gene.";
RL Gene 44:11-16(1986).
RN [3]
RP SEQUENCE OF 432-1145 FROM N.A.
RA Ramirez F.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 963-1418 FROM N.A.
RX MEDLINE=85190534; PubMed=3857598;
RA Cheah K.S.E., Stoker N.G., Griffin J.R., Grosveld F.G., Solomon E.;
RT "Identification and characterization of the human type II collagen
RT gene (COL2A1).";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2555-2559(1985).
RN [5]
RP SEQUENCE OF 1120-1398 FROM N.A.
RX MEDLINE=85306861; PubMed=3840017;
RA Elina K., Maekelae J.K., Vuorio T., Kauppinen S., Knowles J.,
RA Vuorio E.;
RT "Construction and identification of a cDNA clone for human type II
RT procollagen mRNA";
RL Biochem. J. 229:183-188(1985).
RN [6]
RP SEQUENCE OF 1106-1418 FROM N.A.
RX MEDLINE=88067771; PubMed=2825137;
RA Elina K., Vuorio T., Vuorio E.;
RT "Determination of the single polyadenylation site of the human pro
RT alpha 1(II) collagen gene.";
RL Nucleic Acids Res. 15:9499-9504(1987).
RN [7]
RP SEQUENCE OF 1227-1289 FROM N.A.

RX MEDLINE=86104139; PubMed=3002437;
RA Nunez A.M., Francomano C., Young M.F., Martin G.R., Yamada Y.;
RT "Isolation and partial characterization of genomic clones coding for a
RT human pro-alpha 1 (II) collagen chain and demonstration of restriction
RT fragment length polymorphism at the 3' end of the gene.";
RL Biochemistry 24:6343-6348(1985).
RN [18]
RP SEQUENCE OF 1176-1226 FROM N.A.
RX MEDLINE=84118798; PubMed=6320112;
RA Strom C.M., Upholt W.B.;
RT "Isolation and characterization of genomic clones corresponding to the
RT human type II procollagen gene.";
RL Nucleic Acids Res. 12:1025-1038(1984).
RN [9]
RP SEQUENCE OF 35-167 FROM N.A.
RX MEDLINE=89233138; PubMed=2714801;
RA Su M.W., Benson-Chanda V., Vissing H., Ramirez F.;
RT "Organization of the exons coding for pro alpha 1(II) collagen N-
RT propeptide confirms a distinct evolutionary history of this domain of
RT the fibrillar collagen genes.";
RL Genomics 4:438-441(1989).
RN [10]
RP REVIEW ON VARIANTS
RX MEDLINE=91184577; PubMed=2010058;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in collagen genes: causes of rare and some common diseases
RT in humans.";
RL FASEB J. 5:2052-2060(1991).
RN [11]
RP REVIEW ON VARIANTS
RX MEDLINE=97255959; PubMed=9101280;
RA DOI=10.1002/(SICI)1098-1004(1997)9:4<300::AID-HUMU2>3.3.CO;2-8;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [12]
RP VARIANT SER-1074.
RX MEDLINE=90036909; PubMed=2572591;
RA Vissing H., D'Alessio M., Lee B., Ramirez F., Godfrey M.,
RA Hollister D.W.;
RT "Glycine to serine substitution in the triple helical domain of pro-
RT alpha 1 (II) collagen results in a lethal perinatal form of short-
RT limbed dwarfism.";
RL J. Biol. Chem. 264:18265-18267(1989).
RN [13]
RP VARIANT SEDC 1095-GLY--TYR-1330 DEL.
RX MEDLINE=89266907; PubMed=2543071;
RA Lee B., Vissing H., Ramirez F., Rogers D., Rimoin D.L.;
RT "Identification of the molecular defect in a family with
RT spondyloepiphyseal dysplasia.";
RL Science 244:978-980(1989).
RN [14]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=9370826; PubMed=1975693;
RA Ala-Kokko L., Baldwin C.T., Moskowitz R.W., Prockop D.J.;
RT "Single base mutation in the type II procollagen gene (COL2A1) as a
RT cause of primary osteoarthritis associated with a mild
RT chondrodysplasia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6565-6568(1990).
RN [15]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=91086471; PubMed=1985108;
RA Eyre D.R., Weis M.A., Moskowitz R.W.;
RT "Cartilage expression of a type II collagen mutation in an inherited
RT form of osteoarthritis associated with a mild chondrodysplasia.";
RL J. Clin. Invest. 87:357-361(1991).
RN [16]
RP VARIANT HYPOCHONDROGENESIS GLU-984.
RX MEDLINE=93054548; PubMed=1429602;
RA Bogart R., Tiller G.E., Wies M.A., Gruber H.E., Rimoin D.L.,
RA Cohn D.H., Eyre D.R.;
RT "An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II)
RT chain produces hypochondrogenesis.";
RL J. Biol. Chem. 267:22522-22526(1992).
RN [17]
RP VARIANT HYPOCHONDROGENESIS SER-705.
RX MEDLINE=92262484; PubMed=1374906;
RA Horton W.A., Machado M.A., Ellard J., Campbell D., Bartley J.,
RA Ramirez F., Vitale E., Lee B.;
RT "Characterization of a type II collagen gene (COL2A1) mutation
RT identified in cultured chondrocytes from human hypochondrogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4583-4587(1992).
RN [18]
RP VARIANT WS-II ASP-198.
RX MEDLINE=93304428; PubMed=8317498;
RA Koerkoe J., Ritvaniemi P., Haataja L., Kaeerlaeinen H.,
RA Kivirikko K.I., Prockop D.J., Ala-Kokko L.;
RT "Mutation in type II procollagen (COL2A1) that substitutes aspartate
RT for glycine alpha 1-67 and that causes cataracts and retinal
RT detachment: evidence for molecular heterogeneity in the Wagner
RT syndrome and the Stickler syndrome (arthro-ophthalmopathy).";
RL Am. J. Hum. Genet. 53:55-61(1993).
RN [19]
RP VARIANT SEMD CYS-840.
RA Tiller G.E., Weis M.A., Lachman R.S., Cohn D.H., Rimoin D.L.,
RA Eyre D.R.;
RT "A dominant mutation in the type II collagen gene (COL2A1) produces
RT spondyloepimetaphyseal dysplasia (SEMD), Strudwick type.";
RL Am. J. Hum. Genet. 53:A209-A209(1993).
RN [20]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=93282819; PubMed=8507190;
RA Holderbaum D., Malesud C.J., Moskowitz R.W., Haqqi T.M.;
RT "Human cartilage from late stage familial osteoarthritis transcribes
RT type II collagen mRNA encoding a cysteine in position 519.";
RL Biochem. Biophys. Res. Commun. 192:1169-1174(1993).
RN [21]
RP VARIANT SEMD ARG-285.
RX MEDLINE=93252400; PubMed=8486375;
RA Vikkula M., Ritvaniemi P., Vuorio A.F., Kaitila I., Ala-Kokko L.,
RA Peltonen L.;
RT "A mutation in the amino-terminal end of the triple helix of type II
RT collagen causing severe osteochondrodysplasia.";
RL Genomics 16:282-285(1993).
RN [22]
RP VARIANT SEDC CYS-206.
RX MEDLINE=94063862; PubMed=8244341;
RA Williams C.J., Considine E.L., Knowlton R.G., Reginato A., Neumann G.,
RA Harrison D., Buxton P., Jimenez S.A., Prockop D.J.;
RT "Spondyloepiphyseal dysplasia and precocious osteoarthritis in a
RT family with an Arg75-->Cys mutation in the procollagen type II gene
RT (COL2A1).";
RL Hum. Genet. 92:499-505(1993).
RN [23]
RP VARIANT SEDC CYS-920.
RX MEDLINE=93315508; PubMed=8325895;
RA Chan D., Taylor T.K.F., Cole W.G.;
RT "Characterization of an arginine 789 to cysteine substitution in alpha
RT 1 (II) collagen chains of a patient with spondyloepiphyseal
RT dysplasia.";
RL J. Biol. Chem. 268:15238-15245(1993).
RN [24]
RP VARIANT SEDC SER-1128.
RX MEDLINE=93140139; PubMed=8423604;
RA Cole W.G., Hall R.K., Rogers J.G.;
RT "The clinical features of spondyloepiphyseal dysplasia congenita
RT resulting from the substitution of glycine 997 by serine in the alpha
RT 1(II) chain of type II collagen.";
RL J. Med. Genet. 30:27-35(1993).
RN [25]
RP VARIANT STU1 233-ALA--LYS-239 DEL.
RX MEDLINE=95067975; PubMed=7977371;
RA Bogart R., Wilkin D.J., Wilcox W.R., Lachman R.S., Rimoin D.L.,
RA Cohn D.H., Eyre D.R.;

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RT "Expression, in cartilage, of a 7-amino-acid deletion in type II
RT collagen from two unrelated individuals with Knist dysplasia.";
Query Match 100.0%; Score 132; DB 1; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 6
Q28396 PRELIMINARY; PRT; 1418 AA.
AC Q28396;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type II collagen.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97350165; PubMed=9205943; DOI=10.1016/S0945-053X(97)90073-1;
RA Richardson D.W., Dodge G.R.;
RT "Cloning of equine type II procollagen and the modulation of its
RT expression in cultured equine articular chondrocytes.";
RL Matrix Biol. 16:59-64(1997).
DR EMBL; U62528; AAB05773.1; -.
DR PIR; T45467; T45467.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib_collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR ProDom; PD000007; Clg_helix; 5.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR KW Collagen.
SQ SEQUENCE 1418 AA; 134343 MW; 115FCD19EB8696A3 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 7
Q9W7R9 PRELIMINARY; PRT; 1418 AA.
AC Q9W7R9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha type II collagen.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99407244; PubMed=10474166;
RX DOI=10.1002/(SICI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.CO;2-2;
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RA Asahina K., Obara M., Yoshizato K.;
RT "Expression of genes of type I and type II collagen in the formation
RT and development of the blastema of regenerating newt limb.";
RL Dev. Dyn. 216:59-71(1999).
DR EMBL; AB022046; BAA82043.1; -.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib_collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR ProDom; PD01391; Collagen; 18.
DR ProDom; PD000007; Clg_helix; 7.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR KW Collagen.
SQ SEQUENCE 1418 AA; 135066 MW; C19A6E601A2A717E CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 8
Q9W37 PRELIMINARY; PRT; 1420 AA.
AC Q9W37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1 type IIA collagen precursor.
GN Name=COL2A1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sternal;
RA Caixia X., Yongzhi X., Siqi G., Yiyang S.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY046949; AAK98621.1; -.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01410; COLFI; 1.
DR ProDom; PD000007; Clg_helix; 7.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR KW Collagen; Signal.
FT SIGNAL 1 25 Potential.
SQ SEQUENCE 1420 AA; 134998 MW; 88D9AAB17F214FF5 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1420;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 198 ERGPPGPGQARGPFGTGLPGVK 220

RESULT 9
Q91717
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ID	Q91717	PRELIMINARY;	PRT;	1486 AA.
AC	Q91717;			
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Alpha-1 type II collagen.			
GN	NamesCOL2A1;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92011898; PubMed=1918153; DOI=10.1083/jcb.115.2.565;			
RA	Su M.W., Suzuki H.R., Bieker J.J., Solursh M., Ramirez F.;			
RT	"Expression of two nonallelic type II procollagen genes during Xenopus			
RT	laevis embryogenesis is characterized by stage-specific production of			
RT	alternatively spliced transcripts.";			
RL	J. Cell Biol. 115:565-575(1991).			
DR	EMBL; M63595; AAA49678.1; -			
DR	PIR; A40333; A40333.			
DR	PIR; B40333; B40333.			
DR	GO; GO:0005581; C:collagen; IEA.			
DR	GO; GO:0005737; C:cytoplasm; IEA.			
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.			
DR	GO; GO:0006817; P:phosphate transport; IEA.			
DR	Pfam; PF01410; COLF1; 1.			
DR	Pfam; PF01391; Collagen; 18.			
DR	Pfam; PF00093; VWC; 1.			
DR	ProDom; PD000007; C1g_helix; 7.			
DR	ProDom; PD002078; Fib_collagen_C; 1.			
DR	SMART; SM00038; COLF1_1.			
DR	SMART; SM00214; VWC; 1.			
DR	PROSITE; PS01208; VWFC_1; 1.			
DR	PROSITE; PS50184; VWFC_2; 1.			
KW	Collagen.			
SK	SEQUENCE	1486 AA; 142263 MW; 4A4A95772341042F CRC64;		
Query Match 100.0%; Score 132; DB 2; Length 1486;				
Best Local Similarity 100.0%; Pred. No. 4.1e-07;				
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ERGPPGQGARGFGTGPLGVK 23		
Db	267	ERGPPGQGARGFGTGPLGVK 289		
RESULT 10				
Q7ZTI6		PRELIMINARY;	PRT;	1486 AA.
ID	Q7ZTI6			
AC	Q7ZTI6;			
DT	01-JUN-2003	(TrEMBLrel. 24, Created)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	COL2A1 protein.			
GN	NamesCOL2A1;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TSUB=Embryo;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Colling F.S., Wagner L., Shennen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			

RESULT 13
 Q91718 PRELIMINARY; PRT; 1491 AA.
 ID Q91718;
 AC Q91718;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Alpha-1 type II, collagen.
 GN Name=alpha-1 type II, collagen;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92011898; PubMed=1918153; DOI=10.1083/jcb.115.2.565;
 RA Su M.W., Suzuki H.R., Bieker J.J., Solursh M., Ramirez F.;
 RT "Expression of two nonallelic type II procollagen genes during Xenopus
 RT laevis embryogenesis is characterized by stage-specific production of
 RT alternatively spliced transcripts";
 RL J. Cell Biol. 115:565-575(1991).
 DR EMBL; M63596; AAA49679.1; -;
 DR PIR; A40333; A40333.
 DR PIR; B40333; B40333.
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cycloplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF01391; Collagen; 18.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 4.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS0184; VWFC_2; 1.
 KW Collagen.
 SQ SEQUENCE 1491 AA; 142495 MW; 43026FF0F8FB0314 CRC64;

 Query Match 100.0%; Score 132; DB 2; Length 1491;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 ERGPPGPGQARGFPPTGLPGVK 23
 |||||
 DB 270 ERGPPGPGQARGFPPTGLPGVK 292

 RESULT 14
 Q72TM4 PRELIMINARY; PRT; 1491 AA.
 ID Q72TM4;
 AC Q72TM4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE LOC397739 protein.
 GN Names=LOC397739;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC044962; AAA44962.1; -;
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cycloplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR00885; Fib_collagen_C.
 DR InterPro; IPR009041; PMP_SGCI.
 DR InterPro; IPR001007; VWFC_C.
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF01391; Collagen; 18.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 4.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS0184; VWFC_2; 1.
 KW Collagen.
 SQ SEQUENCE 1491 AA; 142492 MW; 2FF7A8DE36D73BC1 CRC64;

 Query Match 100.0%; Score 132; DB 2; Length 1491;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 ERGPPGPGQARGFPPTGLPGVK 23
 |||||
 DB 270 ERGPPGPGQARGFPPTGLPGVK 292

 RESULT 15
 Q6P4Z2 PRELIMINARY; PRT; 1492 AA.
 ID Q6P4Z2;
 AC Q6P4Z2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC75588.
 GN Names=MGC75588;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063191; AAH63191.1; -;
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; Clg helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR000885; Fib_collagen_C.
 DR InterPro; IPR009041; FMP_SGCI.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF01391; Collagen; 16.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 7.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWC_1; 1.
 DR PROSITE; PS0184; VWF_2; 1.
 KW Collagen; Hypothetical protein.
 SQ SEQUENCE 1492 AA; 142696 MW; DB7AF42B94210EB7 CRC64;
 Query Match 100.0%; Score 132; DB 2; Length 1492;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ERGPPGQARGFGTGLPGVK 23
 Db 270 ERGPPGQARGFGTGLPGVK 292
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Search completed: October 8, 2005, 00:26:38
 Job time : 178 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 00:21:07 ; Search time 41 Seconds
(without alignments)
41.876 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGQARGPGTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	132	100.0	1017	4	US-08-468-996-10
3	132	100.0	1060	3	US-08-931-820-3
4	132	100.0	1418	3	US-08-963-825-20
5	132	100.0	1418	3	US-09-010-999-1
6	132	100.0	1418	3	US-09-500-811-20
7	132	100.0	1418	3	US-09-570-573-20
8	132	100.0	1418	3	US-09-548-608-20
9	117	88.6	1442	2	US-08-316-650-12
10	117	88.6	1442	5	PCT-US95-02251-12
11	115	87.1	310	3	US-09-219-849-47
12	115	87.1	492	4	US-08-468-996-12
13	115	87.1	595	3	US-09-219-849-48
14	115	87.1	595	3	US-09-219-849-50
15	115	87.1	822	3	US-09-219-849-49
16	115	87.1	1057	3	US-08-931-820-1
17	115	87.1	1461	4	US-09-585-887-9
18	115	87.1	1461	4	US-09-289-578-9
19	115	87.1	1464	4	US-09-331-347C-21
20	112	84.8	1341	3	US-08-963-825-18
21	112	84.8	1341	3	US-09-500-811-18
22	112	84.8	1341	3	US-09-570-573-18
23	112	84.8	1341	3	US-09-548-608-18
24	109	82.6	684	4	US-09-949-016-8348
25	109	82.6	1024	3	US-08-931-820-2
26	109	82.6	1366	3	US-08-963-825-19
27	109	82.6	1366	3	US-09-500-811-19

28	109	82.6	1366	3	US-09-570-573-19	Sequence 19, Appl
29	109	82.6	1366	3	US-09-548-608-19	Sequence 19, Appl
30	109	82.6	1366	4	US-09-585-887-10	Sequence 10, Appl
31	109	82.6	1366	4	US-09-289-578-10	Sequence 10, Appl
32	109	82.6	1366	4	US-09-949-016-5882	Sequence 5882, Ap
33	92	69.7	546	1	US-08-494-168-10	Sequence 10, Appl
34	92	69.7	1218	4	US-09-949-016-7065	Sequence 7065, Ap
35	92	69.7	1268	4	US-09-949-016-7487	Sequence 7487, Ap
36	92	69.7	1690	4	US-09-949-016-5884	Sequence 5884, Ap
37	91	68.9	938	4	US-09-949-016-9992	Sequence 9992, Ap
38	90	68.2	489	2	US-08-794-795-7	Sequence 7, Appli
39	90	68.2	489	3	US-09-249-200-7	Sequence 7, Appli
40	90	68.2	518	1	US-08-392-367B-2	Sequence 2, Appli
41	90	68.2	518	3	US-08-893-467A-2	Sequence 57, Appl
42	88	66.7	755	4	US-09-919-497-57	Sequence 38, Appl
43	87	65.9	228	3	US-09-219-849-38	Sequence 11119, A
44	87	65.9	260	4	US-09-949-016-11119	Sequence 4, Appli
45	87	65.9	377	3	US-09-342-681C-4	

ALIGNMENTS

RESULT 1

US-08-468-996-11

; Sequence 11, Application US/08468996

; Patent No. 6645504

; GENERAL INFORMATION:

; APPLICANT: Weiner, Howard

; APPLICANT: Miller, Ariel

; APPLICANT: Zheng, Zheng

; APPLICANT: Ahmad, Al-Sabbagh

; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION

; TITLE OF INVENTION: GLUCAGON

; FILE REFERENCE: 1010/18959-US3

; CURRENT APPLICATION NUMBER: US/08/468,996

; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 07/843,752

; PRIOR FILING DATE: 1992-02-28

; PRIOR APPLICATION NUMBER: US 07/460,852

; PRIOR FILING DATE: 1990-02-21

; PRIOR APPLICATION NUMBER: US 07/596,936

; PRIOR FILING DATE: 1990-10-15

; PRIOR APPLICATION NUMBER: US 07/065,734

; PRIOR FILING DATE: 1987-06-24

; PRIOR APPLICATION NUMBER: US 07/454,486

; PRIOR FILING DATE: 1989-12-20

; PRIOR APPLICATION NUMBER: US 07/487,732

; PRIOR FILING DATE: 1990-03-02

; PRIOR APPLICATION NUMBER: US 07/551,632

; PRIOR FILING DATE: 1990-07-10

; PRIOR APPLICATION NUMBER: US 07/379,778

; PRIOR FILING DATE: 1989-07-14

; PRIOR APPLICATION NUMBER: US 07/607,826

; PRIOR FILING DATE: 1990-10-31

; PRIOR APPLICATION NUMBER: US 07/595,468

; PRIOR FILING DATE: 1990-10-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 11

; LENGTH: 492

; TYPE: PRT

; ORGANISM: Bos taurus

US-08-468-996-11

Query Match 100.0%; Score 132; DB 4; Length 492;

Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPGTGLPGVK 23

DB 65 ERGPPGQARGPGTGLPGVK 87

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type II
US-08-931-820-3
Query Match 100.0%; Score 132; DB 3; Length 1060;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23
Db 84 ERGPPGQARGPFGTGLPGVK 106

RESULT 4
US-08-963-825-20
; Sequence 20, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments Carrying Out the
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
US-08-963-825-20
Query Match 100.0%; Score 132; DB 3; Length 1418;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-468-996-10
Query Match 100.0%; Score 132; DB 4; Length 1017;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23
Db 65 ERGPPGQARGPFGTGLPGVK 87

RESULT 3
US-08-931-820-3
; Sequence 3, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96202596.1
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1010/16959-US3
; FILE REFERENCE: 1010/16959-US3
; CURRENT APPLICATION NUMBER: US/08/468,996
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 07/843,752
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; PRIOR APPLICATION NUMBER: US 07/596,936
; PRIOR FILING DATE: 1990-10-15
; PRIOR APPLICATION NUMBER: US 07/065,734
; PRIOR FILING DATE: 1987-06-24
; PRIOR APPLICATION NUMBER: US 07/454,486
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: US 07/487,732
; PRIOR FILING DATE: 1990-03-02
; PRIOR APPLICATION NUMBER: US 07/551,632
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: US 07/379,778
; PRIOR FILING DATE: 1989-07-14
; PRIOR APPLICATION NUMBER: US 07/607,826
; PRIOR FILING DATE: 1990-10-31
; PRIOR APPLICATION NUMBER: US 07/595,468
; PRIOR FILING DATE: 1990-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-468-996-10
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Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 5
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen
US-09-010-999-1

Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 6
US-09-500-811-20
; Sequence 20, Application US/09500811
; Patent No. 6323314

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; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/187,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C.
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
US-09-500-811-20

Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 7
US-09-570-573-20
; Sequence 20, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
;
US-09-548-608-20

Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred.No.3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0

QY 1 ERGPPGQGARGFGTGLPGVK 23
   |||||
DB 196 ERGPPGQGARGFGTGLPGVK 218

RESULT 9
US-08-316-650-12
; Sequence 12, Application US/08316650
; Patent No. 5942496
;
GENERAL INFORMATION:
; APPLICANT: Bonadio, Jeffrey
; APPLICANT: Roessler, Blake J.
; APPLICANT: Goldstein, Steven A.
; APPLICANT: Lin, Wushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: FOR STIMULATING BONE CELLS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,650
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 514
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/199,780
; FILING DATE: 30-SEP-1994
;
ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UMIC:008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
;
INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 amino acids
; TYPE: amino acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-316-650-12

Query Match 88.6%; Score 117; DB 2; Length 1442;
Best Local Similarity 91.3%; Pred. No. 2.7e-06;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ERGPPGPGARGFGTPTGLPGVK 23
Db 220 ERGLPGMGARGFGTPTGLPGVK 242

RESULT 10

PCT-US95-02251-12
Sequence 12, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING BONE
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994

CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC009p--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679

TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-02251-12

Query Match 88.6%; Score 117; DB 5; Length 1442;
Best Local Similarity 91.3%; Pred. No. 2.7e-06;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ERGPPGPGARGFGTPTGLPGVK 23
Db 220 ERGLPGMGARGFGTPTGLPGVK 242

RESULT 11

US-09-219-849-47
Sequence 47, Application US/09219849
Patent No. 6150081
GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.

TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
FILE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 310
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-219-849-47

Query Match 87.1%; Score 115; DB 3; Length 310;
Best Local Similarity 87.0%; Pred. No. 1e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ERGPPGPGARGFGTPTGLPGVK 23
Db 64 ERGPPGPGARGFGTPTGLPGVK 86

RESULT 12

US-08-468-996-12
Sequence 12, Application US/08468996
Patent No. 6645504
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zheng
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
TITLE OF INVENTION: GLUCAGON
FILE REFERENCE: 1010/16959-US3
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 07/843,752
PRIOR FILING DATE: 1992-02-28
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR FILING DATE: 1990-02-21
PRIOR APPLICATION NUMBER: US 07/596,936
PRIOR FILING DATE: 1990-10-15
PRIOR APPLICATION NUMBER: US 07/065,734
PRIOR FILING DATE: 1987-06-24
PRIOR APPLICATION NUMBER: US 07/454,486
PRIOR FILING DATE: 1989-12-20
PRIOR APPLICATION NUMBER: US 07/487,732
PRIOR FILING DATE: 1990-03-02
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: US 07/379,778
PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
PRIOR FILING DATE: 1990-10-31
PRIOR APPLICATION NUMBER: US 07/595,468
PRIOR FILING DATE: 1990-10-10
NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-468-996-12
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Query Match      87.1%; Score 115; DB 4; Length 492;
Best Local Similarity 87.0%; Pred. No. 1.6e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 65 ERGPPGPGQARGLPGTAGLPGMK 87
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RESULT 13
US-09-219-849-48
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; Sequence 48, Application US/09219849
; Patent No. 6150081
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: VAN HEERDE, GEORGE V.
```

```
; APPLICANT: VAN RIJN, ALEXIS C.
```

```
; APPLICANT: BOUMSTRA, JAN B.
```

```
; APPLICANT: DE WOLF, FREDERIK A.
```

```
; APPLICANT: MOOBROEK, ANDREAS
```

```
; APPLICANT: WERTEN, MARC W.T.
```

```
; APPLICANT: WIND, RICHELE D.
```

```
; APPLICANT: VAN DEN BOSCH, TANJA J.
```

```
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
```

```
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
```

```
; TITLE OF INVENTION: PREPARATION THEREOF
```

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; FILE REFERENCE: 2728-2
```

```
; CURRENT APPLICATION NUMBER: US/09/219,849
```

```
; CURRENT FILING DATE: 1998-12-23
```

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; NUMBER OF SEQ ID NOS: 50
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 48
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; LENGTH: 595
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; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: amino acid sequence
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```
US-09-219-849-48
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```
Query Match      87.1%; Score 115; DB 3; Length 595;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 64 ERGPPGPGQARGLPGTAGLPGMK 86
|||||
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RESULT 14
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US-09-219-849-50
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; Sequence 50, Application US/09219849
```

```
; Patent No. 6150081
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: VAN HEERDE, GEORGE V.
```

```
; APPLICANT: VAN RIJN, ALEXIS C.
```

```
; APPLICANT: BOUMSTRA, JAN B.
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; APPLICANT: DE WOLF, FREDERIK A.
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; APPLICANT: MOOBROEK, ANDREAS
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; APPLICANT: WERTEN, MARC W.T.
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```
; APPLICANT: WIND, RICHELE D.
```

```
; APPLICANT: VAN DEN BOSCH, TANJA J.
```

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; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
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; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
```

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; TITLE OF INVENTION: PREPARATION THEREOF
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; FILE REFERENCE: 2728-2
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; CURRENT APPLICATION NUMBER: US/09/219,849
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; CURRENT FILING DATE: 1998-12-23
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; NUMBER OF SEQ ID NOS: 50
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 50
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; LENGTH: 595
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; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: amino acid sequence
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US-09-219-849-50
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Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 64 ERGPPGPGQARGLPGTAGLPGMK 86
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US-09-219-849-49
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; Sequence 49, Application US/09219849
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; Patent No. 6150081
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; GENERAL INFORMATION:
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; APPLICANT: VAN HEERDE, GEORGE V.
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; APPLICANT: VAN RIJN, ALEXIS C.
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; APPLICANT: BOUMSTRA, JAN B.
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; APPLICANT: DE WOLF, FREDERIK A.
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; APPLICANT: MOOBROEK, ANDREAS
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; APPLICANT: WERTEN, MARC W.T.
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; APPLICANT: WIND, RICHELE D.
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; APPLICANT: VAN DEN BOSCH, TANJA J.
```

```
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
```

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; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
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; TITLE OF INVENTION: PREPARATION THEREOF
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; FILE REFERENCE: 2728-2
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; CURRENT APPLICATION NUMBER: US/09/219,849
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; CURRENT FILING DATE: 1998-12-23
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; NUMBER OF SEQ ID NOS: 50
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; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: amino acid sequence
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US-09-219-849-49
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Best Local Similarity 87.0%; Pred. No. 2.7e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 64 ERGPPGPGQARGLPGTAGLPGMK 86
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Search completed: October 8, 2005, 00:31:02
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Job time : 42 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2005, 00:17:47 ; Search time 166 Seconds
(without alignments)

57.641 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGQARGFGPTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	132	100.0	24	16	US-10-674-065-6
3	132	100.0	24	16	US-10-674-065-7
4	132	100.0	24	16	US-10-674-065-8
5	132	100.0	24	16	US-10-674-065-9
6	132	100.0	24	16	US-10-674-065-13
7	132	100.0	24	16	US-10-674-065-14
8	132	100.0	84	16	US-10-674-065-1
9	132	100.0	84	16	US-10-674-065-18
10	132	100.0	85	16	US-10-674-065-11
11	132	100.0	85	16	US-10-674-065-12

12	132	100.0	243	16	US-10-723-860-1085	Sequence 1085, Ap
13	132	100.0	492	16	US-10-639-286-11	Sequence 11, Appl
14	132	100.0	1014	14	US-10-194-441A-1	Sequence 1, Appli
15	132	100.0	1017	16	US-10-639-286-10	Sequence 10, Appl
16	132	100.0	1418	14	US-10-058-124-20	Sequence 20, Appl
17	132	100.0	1418	16	US-10-468-091-5	Sequence 5, Appli
18	132	100.0	1487	18	US-10-756-149-4739	Sequence 4739, Ap
19	132	92.4	1014	14	US-10-194-441A-48	Sequence 48, Appl
20	122	92.4	1487	16	US-10-468-091-6	Sequence 6, Appli
21	115	87.1	102	14	US-10-232-175-15	Sequence 15, Appl
22	115	87.1	261	14	US-10-232-175-16	Sequence 16, Appl
23	115	87.1	310	15	US-10-342-331-47	Sequence 47, Appl
24	115	87.1	492	16	US-10-639-286-12	Sequence 12, Appl
25	115	87.1	501	14	US-10-232-175-17	Sequence 17, Appl
26	115	87.1	595	15	US-10-342-331-48	Sequence 48, Appl
27	115	87.1	595	15	US-10-342-331-50	Sequence 50, Appl
28	115	87.1	822	15	US-10-342-331-49	Sequence 49, Appl
29	115	87.1	1014	17	US-10-901-816A-5	Sequence 5, Appli
30	115	87.1	1014	17	US-10-901-816A-6	Sequence 6, Appli
31	115	87.1	1014	17	US-10-901-816A-7	Sequence 7, Appli
32	115	87.1	1014	17	US-10-901-816A-8	Sequence 8, Appli
33	115	87.1	1014	17	US-10-901-816A-9	Sequence 9, Appli
34	115	87.1	1014	17	US-10-901-816A-10	Sequence 10, Appl
35	115	87.1	1014	17	US-10-901-816A-11	Sequence 11, Appl
36	115	87.1	1014	17	US-10-901-816A-13	Sequence 13, Appl
37	115	87.1	1057	15	US-10-104-889-16	Sequence 16, Appl
38	115	87.1	1057	15	US-10-104-889-20	Sequence 20, Appl
39	115	87.1	1057	18	US-10-104-793-16	Sequence 16, Appl
40	115	87.1	1057	18	US-10-104-793-20	Sequence 20, Appl
41	115	87.1	1107	15	US-10-104-889-11	Sequence 11, Appl
42	115	87.1	1107	18	US-10-104-793-11	Sequence 11, Appl
43	115	87.1	1169	15	US-10-104-889-6	Sequence 6, Appli
44	115	87.1	1169	18	US-10-104-793-6	Sequence 6, Appli
45	115	87.1	1171	15	US-10-104-889-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-674-065-3
; Sequence 3, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-674-065-3

Query Match 100.0%; Score 132; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGFGPTGLPGVK 23
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DB 1 ERGPPGQARGFGPTGLPGVK 23

RESULT 2

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US-10-674-065-6
; Sequence 6, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (18)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-6
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ERGPPGPGARGPFGTGLPGVK 23
Db 2 ERGPPGPGARGPFGTGLPGVK 24
RESULT 3
US-10-674-065-7
; Sequence 7, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-8
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ERGPPGPGARGPFGTGLPGVK 23
Db 2 ERGPPGPGARGPFGTGLPGVK 24
RESULT 4
US-10-674-065-8
; Sequence 8, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
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; OTHER INFORMATION: hydroxylated proline
US-10-674-065-8
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 ERGPPGPGARGPFGTGLPGVK 24
RESULT 5
US-10-674-065-9
; Sequence 9, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-9
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ERGPPGPGARGPFGTGLPGVK 23
Db 2 ERGPPGPGARGPFGTGLPGVK 24

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/ PRIOR FILING DATE: 2002-09-30
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 9
/ LENGTH: 24
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)
/ OTHER INFORMATION: hydroxylated proline
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/ NAME/KEY: MOD_RES
/ LOCATION: (15)
/ OTHER INFORMATION: hydroxylated proline
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (18)
/ OTHER INFORMATION: hydroxylated proline
US-10-674-065-9

Query Match          100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 ERGPPGPGQARGPFGTGPLGVK 24
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RESULT 6
US-10-674-065-13
/ Sequence 13, Application US/10674065
/ Publication No. US20040122209A1
/ GENERAL INFORMATION:
/ APPLICANT: POOLE, A. ROBIN
/ TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
/ FILE REFERENCE: 079328-0105
/ CURRENT APPLICATION NUMBER: US/10/674,065
/ CURRENT FILING DATE: 2003-09-30
/ PRIOR APPLICATION NUMBER: 60/414,332
/ PRIOR FILING DATE: 2002-09-30
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 13
/ LENGTH: 24
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-674-065-13

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Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Publication No. US20040122209A1
/ GENERAL INFORMATION:
/ APPLICANT: POOLE, A. ROBIN
/ TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
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/ TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
/ FILE REFERENCE: 079328-0105
/ CURRENT APPLICATION NUMBER: US/10/674,065
/ CURRENT FILING DATE: 2003-09-30
/ PRIOR APPLICATION NUMBER: 60/414,332
/ PRIOR FILING DATE: 2002-09-30
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/ SOFTWARE: PatentIn Ver. 3.2
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/ OTHER INFORMATION: hydroxylated proline
/ FEATURE:
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/ LOCATION: (21)
/ OTHER INFORMATION: hydroxylated proline
US-10-674-065-14

Query Match          100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGPLGVK 23
Db 2 ERGPPGPGQARGPFGTGPLGVK 24
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RESULT 8
US-10-674-065-1
/ Sequence 1, Application US/10674065
/ Publication No. US20040122209A1
/ GENERAL INFORMATION:
/ APPLICANT: POOLE, A. ROBIN
/ TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
/ FILE REFERENCE: 079328-0105
/ CURRENT APPLICATION NUMBER: US/10/674,065
/ CURRENT FILING DATE: 2003-09-30
/ PRIOR APPLICATION NUMBER: 60/414,332
/ PRIOR FILING DATE: 2002-09-30
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 1
/ LENGTH: 84
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-674-065-1

Query Match          100.0%; Score 132; DB 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGPLGVK 23
Db 25 ERGPPGPGQARGPFGTGPLGVK 47
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; Sequence 18, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
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; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
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; LOCATION: (9)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
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; LOCATION: (66)
; OTHER INFORMATION: hydroxylated proline
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; NAME/KEY: MOD_RES
; LOCATION: (75)
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; LOCATION: (81)
; OTHER INFORMATION: hydroxylated proline
; US-10-674-065-18

RESULT 9
US-10-674-065-18
; Sequence 18, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (30)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (42)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (45)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (54)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (66)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (81)
; OTHER INFORMATION: hydroxylated proline
; US-10-674-065-18

Query Match 100.0%; Score 132; DB 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGTLPGVK 23
| | | | | | | | | | | | | | | | | | | |
Db 26 ERGPPGPGQARGFGPTGTLPGVK 48
| | | | | | | | | | | | | | | | | | | |

RESULT 10
US-10-674-065-11
; Sequence 11, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-674-065-11

Query Match 100.0%; Score 132; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGTLPGVK 23
| | | | | | | | | | | | | | | | | | | |
Db 26 ERGPPGPGQARGFGPTGTLPGVK 48
| | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-674-065-12
; Sequence 12, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (30)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (42)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (45)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (54)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (66)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (81)
; OTHER INFORMATION: hydroxylated proline
; US-10-674-065-12
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FEATURE:
NAME/KEY: MOD RES
LOCATION: (12)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (21)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (30)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (42)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (45)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (66)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (75)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (81)
OTHER INFORMATION: hydroxylated proline
US-10-674-065-12

Query Match 100.0%; Score 132; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGGARGPGTGLPGVK 23
Db 26 ERGPPGPGGARGPGTGLPGVK 48

RESULT 12
US-10-723-860-1085
Sequence 1085, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1085
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-1085

Query Match 100.0%; Score 132; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGGARGPGTGLPGVK 23
Db 167 ERGPPGPGGARGPGTGLPGVK 189

RESULT 13
US-10-639-286-11
Sequence 11, Application US/10639286
Publication No. US20040115217A1
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zhengyi
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF AUTOIMMUNE DISEASE
FILE REFERENCE: 01010/1006959-US7
CURRENT APPLICATION NUMBER: US/10/639,286
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 08/472,017
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 07/843,752
PRIOR FILING DATE: 1992-02-28
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR FILING DATE: 1990-03-21
PRIOR APPLICATION NUMBER: US 07/596,936
PRIOR FILING DATE: 1990-10-15
PRIOR APPLICATION NUMBER: US 07/065,734
PRIOR FILING DATE: 1987-06-24
PRIOR APPLICATION NUMBER: US 07/454,486
PRIOR FILING DATE: 1989-12-20
PRIOR APPLICATION NUMBER: US 07/487,732
PRIOR FILING DATE: 1990-03-02
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: US 07/379,778
PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 492
TYPE: PRT
ORGANISM: Bos taurus
US-10-639-286-11

Query Match 100.0%; Score 132; DB 16; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGGARGPGTGLPGVK 23
Db 65 ERGPPGPGGARGPGTGLPGVK 87

RESULT 14
US-10-194-441A-1
Sequence 1, Application US/10194441A
Publication No. US20030148944A1
GENERAL INFORMATION:
APPLICANT: Holmdahl, Rikard
APPLICANT: Engstrom, Jan Ake
APPLICANT: Kihlberg, Jan
APPLICANT: Burkhardt, Harald
TITLE OF INVENTION: TRIPLE POLYPEPTIDE COMPLEXES
FILE REFERENCE: 11145-010001
CURRENT APPLICATION NUMBER: US/10/194,441A
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US 60/305,048
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 87

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-441A-1

Query Match      100.0%; Score 132; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGPFGTGLPGVK 23
DB      65 ERGPPGPGQARGPFGTGLPGVK 87

RESULT 15
US-10-639-286-10
; Sequence 10, Application US/10639286
; Publication No. US20040115217A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zhengyi
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF AUTOIMMUNE DISEASE
; FILE REFERENCE: 01010/1006959-US7
; CURRENT APPLICATION NUMBER: US/10/639,286
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 08/472,017
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 07/843,752
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; PRIOR APPLICATION NUMBER: US 07/596,936
; PRIOR FILING DATE: 1990-10-15
; PRIOR APPLICATION NUMBER: US 07/065,734
; PRIOR FILING DATE: 1987-06-24
; PRIOR APPLICATION NUMBER: US 07/454,486
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: US 07/487,732
; PRIOR FILING DATE: 1990-03-02
; PRIOR APPLICATION NUMBER: US 07/551,632
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: US 07/379,778
; PRIOR FILING DATE: 1989-07-14
; PRIOR APPLICATION NUMBER: US 07/607,826
; PRIOR FILING DATE: 1990-10-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-639-286-10

Query Match      100.0%; Score 132; DB 16; Length 1017;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGPFGTGLPGVK 23
DB      65 ERGPPGPGQARGPFGTGLPGVK 87
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Search completed: October 8, 2005, 00:30:14
Job time : 167 secs